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<220> misc feature
 <221> 18-24, 32-38, 34-40, 31-41, 51-57
 <222> N-Myristoylation Site.
 <220>
 <221> misc feature
 <222> 22-26, 50-54, 113-117
 <223> Casein Kinase II Phosphorylation Site.

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 1 5 10 15
 Gly Gln Gly Leu Leu Leu Thr Leu Glu Glu His Ile Ala His Phe
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 Leu Gly Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile
 35 40 45
 Lys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
 50 55 60
 Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser
 65 70 75
 Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
 80 85 90
 His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu
 95 100 105
 Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Lys
 110 115

<110> 7
 <211> 756
 <112> DNA
 <113> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 <223> Signal Peptide

<220>
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 <222> 4-10, 5-11, 47-53, 170-176, 176-182
 <223> N-Myristoylation Site.

<220>
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 <222> 44-85
 <223> G-protein Coupled Receptors Proteins.

<220>
 <221> misc feature
 <222> 54-65
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

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 <222> 82-86
 <223> Casein Kinase II Phosphorylation Site.

<220>
 <221> TRANSMEM
 <222> 86-103, 60-75
 <223> Transmembrane Domain

<220>
 <221> misc_feature
 <222> 144-151
 <223> Tyrosine Kinase Phosphorylation Site.

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Phe	Val	Ser	Gly	Phe	Leu	Leu	Phe	Arg	Ser	Leu	Pro	Arg	His	Thr
				35					40					45
Phe	Gly	Leu	Val	Gln	Ser	Lys	Leu	Phe	Pro	Phe	Tyr	Phe	His	Ile
				50					55					60
Ser	Met	Gly	Cys	Ala	Phe	Ile	Asn	Leu	Cys	Ile	Leu	Ala	Ser	Gln
				65					70					75
His	Ala	Trp	Ala	Gln	Leu	Thr	Phe	Trp	Glu	Ala	Ser	Gln	Leu	Tyr
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Leu	Leu	Phe	Leu	Ser	Leu	Thr	Leu	Ala	Thr	Val	Asn	Ala	Arg	Trp
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Leu	Glu	Pro	Arg	Thr	Thr	Ala	Ala	Met	Trp	Ala	Leu	Gln	Thr	Val
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Glu	Lys	Glu	Arg	Gly	Leu	Gly	Gly	Glu	Val	Pro	Gly	Ser	His	Gln
				125					130					135
Gly	Pro	Asp	Pro	Tyr	Arg	Gln	Leu	Arg	Glu	Lys	Asp	Pro	Lys	Tyr
				140					145					150
Ser	Ala	Leu	Arg	Gln	Asn	Phe	Phe	Arg	Tyr	His	Gly	Leu	Ser	Ser
				155					160					165
Leu	Cys	Asn	Leu	Gly	Cys	Val	Leu	Ser	Asn	Gly	Leu	Cys	Leu	Ala
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Gly	Leu	Ala	Leu	Glu	Ile	Arg	Ser	Leu						
				185										

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 (211): 1508
 (212): DNA
 (213): Homo sapiens

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 caggatcaac agctttaaaq gcagaaacct cagagagact tctactgtg 350
 ctctgtgatg tgacgaaccc agagaatttc aacaggaactg cccagtggtt 400

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<210> 10
 <211> 319
 <212> PRT
 <213> Homo sapiens

<210>
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 <212> 1-17
 <213> Signal Peptide

<220>
 <221> misc_feature

<222> 36-47, 108-113, 186-171, 192-203, 207-212
 <223> N-myristoylation Sites.

<220>
 <221> misc_feature
 <222> 39-42
 <223> Glycosaminoglycan Attachment Site.

<220>
 <221> TRANSMEM
 <222> 136-152
 <223> Transmembrane Domain

<220>
 <221> misc_feature
 <222> 161-163, 187-190 and 253-256
 <223> N-glycosylation Sites.

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 35 40 45
 Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
 50 55 60
 Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
 65 70 75
 Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
 80 85 90
 Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
 95 100 105
 Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
 110 115 120
 Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
 125 130 135
 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
 140 145 150
 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
 155 160 165
 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
 170 175 180
 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
 185 190 195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys	200	205	210
Pro	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala	215	220	225
His	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu	230	235	240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser	245	250	255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His	260	265	270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys	275	280	285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala	290	295	300
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Pro Lys Ala Val

<310> 11
 <311> 2720
 <312> DNA
 <313> Homo sapiens

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 ctacgatgct cccaatccaa gggctctggag gggtgcctgt gactccagag 2550
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 cctctggccc gccccgcagg gggcttggag ggtcggacgg caagtcctgc 2650
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 ttgatttgc ctaacgcgaa 2720

4100: 12
 4110: 639
 4115: PRT
 4120: Homo sapiens

4220:
 4221: TRANSMEM
 4222: 21-40 and 84-105
 4223: Transmembrane Domain (type II)

4400: 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
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 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Gln Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Gln Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val Ser	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe Glu	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His Leu	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly Asn	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr Ser	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp Thr	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu Phe			

395	400	405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala	
410	415	420
Val Glu Lys Val	Thr Gln His Ile His Gly Leu Ser Gly Lys Lys	
425	430	435
Asp Gly Leu Val	Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe	
440	445	450
Thr His Leu Gly	Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr	
455	460	465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu	
470	475	480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg	
485	490	495
Thr His Leu Leu	Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val	
500	505	510
Gly Glu Leu Ala	His Gly Arg Phe Ser Ala Lys Met Asp His Leu	
515	520	525
Val Cys Phe Leu	Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly	
530	535	540
Leu Pro Ala Ser	His Met Glu Leu Ala Gln Glu Leu Met Glu Thr	
545	550	555
Cys Tyr Gln Met	Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu	
560	565	570
Ile Val His Phe	Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val	
575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr	
590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys	
605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe	
620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln	
635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe	
650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp	
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Pro Asn Leu Leu	Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala	
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
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<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
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<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgaagt gtttggcctc ggtc 44

<210> 16
<211> 1104
<212> DNA
<213> Homo sapiens

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<10> 17
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<218> sig_peptide
<222> 1-43
<223> Signal peptide.

<220>
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<222> 19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 19-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

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Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
          20             25             30

Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
          35             40             45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
          50             55             60

Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
          65             70             75

Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
          80             85             90

Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
          95             100            105

Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
          110            115            120

Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
          125            130            135

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

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140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp	
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala	
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His	
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His	
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly	
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu	
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe	
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg	
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly	
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu	
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp	
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser	
320	325	

<210> 18

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 18

gcggaacgctt cgaggagttc tgg 23

<210> 19

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcaatgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 10
ctttctcagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccact cccccaagcc cctttaccta tgctqctgct 50
aagctgctg ctgctgctgc tgetgettta aggetcatgc ttggagtggg 100
gctgttggg tgcacagaaa gtctctttct ccactgacgc cccatcagg 150
gattgacct tctttccccc ttcttttttg tgtctctctg ctcatcgccc 200
tctcatgacc tgcagccaaag cccagccccg tggggaaggg gagaaagtgg 250
gggatgcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatccaa agatattaag gccctgttca ttaagaaatt gtcccttcc 400
cctctgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacattta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 21
<211> 77
<212> PRT
<213> Homo sapiens

<210>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<10> Growth factor and cytokines receptors family.

<10> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<110> 23

<111> 1883

<112> DNA

<113> Homo sapiens

<400> 23

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tagcggacaaa aggagcatgt cccgcgcggg gaaggcccggt cctcgggcgg 100

ccataagggt cgggtgcgcg ctgggcgcgc gcgcgcctcc tgcgcgcgcg 150

ggctcggggg aggcgcgcta ggcagtgag cgcgcgctcg cccgcagggc 200

ccgggcgcgc agcatggagc caccgcgagc cgggcggggc cgcgcgcagc 250

cgcgcgtgtt gctgcgcctc tgcgtgttag cgcgcctgc gctgcctgga 300

gggcgcggcg cgcgcgcgc cgcgcgcctg cccgcgcgtt gcaagcacga 350

tgggcgcgc cgcgcgcctg gcagggcggc ggcgcgcgc gagggcgaagg 400

tgggtgtgcg cgcgcgcgaa ctgcgcgcgc tctgcgcgc agatactctg 450

cccaaccgca cggtcaccc tgcctgtagt aacaataaga tatccgagct 500

gaagaatgcc tcattttctg ggttaagtt ccttgaaaga ttggacctcc 550

gaaacaattc tattagtagt atagatccag gtgcctttctg gggactgtca 600

tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650

agacatattt cgcgcgcctc ccaatctggt cgggcctaac cttcggggga 700

atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750

cggctcttgg aatccagac tgcgtatctt ttgtgtgact gtaacatact 800

gtgcgtgcct cgcgcgcctc aggcgcgcgc cgcgcgcctc cgcgcgcctc 850

tttaaa aaattttttt tgaattttttt gttttttttt ttgttttttt 2350
 attttgtttt ttaagacaat agatgtttt catggggccc taaaagtatc 2400
 attttttt ggactggc ctgcacagcc tagtgagaaa gtcaacctg 2450
 atttttggtg ttttaataag caagctgtat atcaaaattt ttggcagaaa 1500
 atttttatat gtcatatata tttttttaaa aaaagtattt cattgaagca 1550
 atttttatga aagcattttt actgattttt aaaattgggtg ctttagatat 1600
 atttttatac actgtattga agcaaataga ggaggacaaa ctccagcacc 1650
 atttttgaac cacatttttt tcaattagct ttctgtgggc atgtgtaatt 1700
 attttttctg cggttttttt tctcacagta cttttttctt gtcttgtccc 1750
 tcaatttatat cacaaacaat attccagtc ttttaattggc tgcataataa 1800
 ctgtttcaac aggtgttagg tgtttctggtt tagtgtgagc actcaataaa 2850
 tattgaatga atgaacjaaa aaaaaaaaaa aaa 2883

<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<20>
 <21> sig_peptide
 <22> 1-33
 <23> Signal peptide.

<20>
 <21> TRANSMEM
 <22> 13-40
 <23> Transmembrane domain (type II).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

Asp	Tyr	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
				95					100					105	
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	
				110					115					120	
Asp	Arg	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
				125					130					135	
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	
				140					145					150	
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
				155					160					165	
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	
				170					175					180	
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	
				185					190					195	
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	
				200					205					210	
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	
				215					220					225	
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Gln	
				230					235					240	
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	
				245					250					255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
				260					265					270	
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Gln	
				275					280					285	
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Gln	Lys	Asn	Met	Ile	His	
				290					295					300	
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln	
				305					310					315	
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg	
				320					325					330	
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	
				335					340					345	
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp	
				350					355					360	
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	
				365					370					375	
Tyr	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro	

380	385	390
His Asp Glu Arg Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly Phe	
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp Val	
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu Thr	
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val Glu	
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp	Val Ile Phe Val Ala Glu	
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser Lys	
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile	Ala Ser Asn Ile Met Leu	
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys Ala	
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr Arg	
515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn Ile	
530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly Met	
545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr Gly	
560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp Lys	
575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser Leu	
590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile Tyr	
605	610	615

Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<218> Synthetic construct

<400> 25

gaagactcac caatctggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

gaagtgaaaag gaagctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 17

atcaaggaga agaactcac ggtacgggat accaggtgtg ttatcctaa 50

<210> 18

<211> 533

<212> DNA

<213> Homo sapiens

<400> 18

acgtgaggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50

ctcaccgggg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100

gcagaggttt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

aaaaacaaaa cattcgtctt ttgggagAAC agattatTTT gactgagcaa 200

cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaatat ctcttggaac gacaacacga gtttgtgtgt 300

gtgtgttgat ggagagtage ttagtagtat ctccatcttt ttttttggtc 350

actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

ctgctttcag gttcccttat atctgaataa aggagtgtgg gcagacactt 450

tttggaagag tctgtctggg tcatcctggt agaagcccca ttaggttcac 500

tatcaactgc ttaaggttat tactgagaag caactgcagag cttgtgagaa 550

ttttgggttg gttgtgtgaa ttttactgaa tttttgttt attttgcatd 600
 atpattgaagc cactggtgaca ttttacttcaq naggacttga ggaaggtgaa 650
 gttggagggag agactgtctct tatgtgtgaa ttc 683

<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu
 1 5 10 15
 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
 80

<410> 30
 <411> 2128
 <412> DNA
 <413> Homo sapiens

<400> 30
 ctgttgtctt tgtttcagcc gcagtgcaca ctggtgtcct gaggtgtctt 50
 tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100
 tccatggatt cctctgttaa gaccgtgccc atgccagtga cggtaaccgc 150
 caccaccatc acaaccacca cgacgtcacc ttctgggctg gggtcaccca 200
 tgatcgtggg gtccctctgg gccctgacac agcccttggg tctccttggc 250
 ctgtgtcagc tgggtgtctc ctgcgtggcc ttctcgttgg tggctagcgt 300
 gggcgcttgg accgggttca tctgcaactg gtccatgttc acctggtgct 350
 tttgtttctc cgttgccttg atcatcttca tctgtggagt gtgtgggctc 400
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ctatgcggaa ctctctctaac tctcgaact ccttatctac ctacacact 500
 atgtccagtt cctgtccaac acccgttct ggtaccacgc cctgcgcgc 550
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 gacccgggac ccggccggcg agatcactgg ctatctggcc accgtacccg 650
 ggttgtgaa ggtgttagg accttcgtt cctccatcat cttcgcgctc 700
 atcagcgacc ccaacctgtt ccagcaccag ccggccctgg agtggtgct 750
 ggcggtgtac gccatctgt tcatcttag gcccatcgcc atcctgtga 800
 acctggggga gtgcaccaac gtgtaccca tcccttccc cagcttccctg 850
 tcggggctgg ccttgctgtc tgtctctc tatgcaccc ccttggttct 900
 ctggccctcc taccagttcg atgagaagta tggcgccag cctcgggcct 950
 cgagagatgt aagctgcagc ccgagccatg cctactacgt gtgtgcctgg 1000
 gacgcgcgac tggctgtggc catctgacg gccatcaac tactggcgta 1050
 tgtggctgac ctggtgcact ctgcacact ggtttttgc aaggtctaag 1100
 actctccaa gaggtcccg ttcctctcc aacctcttg ttctctctgc 1150
 ccgagtttcc ttatggagt actcttccc tcggcttcc ctctgttcc 1200
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 tgcactctaa ccagttcttg gatgcattt cttcttccc ttctctctg 1300
 ctgttctctt cctgtgtgt tttgttgccc acatctggt tccacccctg 1350
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 gattctcact ctgtggccc ggttgagtg cagtggcgcg atctcagct 1450
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 gtgtgtgtgt gtgtgtgtt ggagctgag ggtgggtag ctggggattg 1850
 ggcctctct ctcacagtgg aaggaagtgt gcatgtact tcccttttaa 1900

caaaac atatatatat atatattt m aigt caataa ttcccaatgg 1950
 g aaaggga ttaaggcaag accttgggtc cctaggcccc goctgggaact 2000
 caa ttggc agaaattggc tccagaattt ttgcagaggt taacagaacac 2050
 caatccca gaggccatct taaaggaagc aggggctgga tgcctttcat 2100
 tccactatt ctctatgta tgaaaaaa 2126

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Thr
1				5					10					15
Ser	Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg
				20					25					30
Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val
				35					40					45
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp
				50					55					60
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys
				65					70					75
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu
				80					85					90
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe
				95					100					105
Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr
				110					115					120
Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp
				125					130					135
His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala
				140					145					150
Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile
				155					160					165
Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu
				170					175					180
Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn
				185					190					195
Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Gln	Trp	Cys	Val	Ala	Val	Tyr
				200					205					210

Arg	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu
				215					220					225
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu
				230					235					240
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu
				245					250					255
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln
				260					265					270
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr
				275					280					285
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr
				290					295					300
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala
				305					310					315
His	Leu	Val	Phe	Val	Lys	Val								
				320										

<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

<400> 32
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 ttccaccatg ttggccagggc tggctcttgaa ctctgtgacct catgatccgc 100
 tcacctcggc ctcccaaagt gctgggatta caggaatgag ccactgacgc 150
 ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200
 taaacattgg gcactacagt gacccaaaaca gactgaattc cccaagagcc 250
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300
 ttattactca ctatgactaa gggtcacaaa tggggtaagt tgatggagag 350
 tgatttgta agagactaca gagggaggac agactaccaa gagggggggc 400
 aggaaagctc ctctgacgag gtgggtatttc agccaaaact ggaagaatga 450
 gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500
 cactcactac accttggcct gagaaaatag catgggattg gaggaggctg 550
 ggggaacacc acctctgccg acctgggcag gaggcattga gggcttgaga 600
 aaagggaatg acagtgcag tagaaaggac agggtaggag cagggaactt 650
 ttagctggaa tcattaggtc ttatcaacag atatgggaa gaaagagag 700

gcttcaattg atgttaatgc ttaggtttgg agcagatta gat ttttag 750
 tggg tggtag tgcacaaggaa agaggtcagg aagcaggggc agaatgtagg 800
 agaatgtgtg ggggttttgt ttcattcttg ccaggtctgc cggaatgtgg 850
 atcgaagac caagaggagg acaaggggc agaggggaag ggaatcttaa 900
 aqaagtctg gatgcacac tcttcttctt tcttctctt cctctctct 950
 agaggtctca ctgtgggtt ttcatttctt ggcctgcctc catctctct 1000
 ggggtctggg aaagtggagg attagctgaa gttttgcttc tggggcctg 1050
 tctgaatctc cattgcttct tgggaggaca taatcactt gtcctagctt 1100
 ctatcatct tacatttccc tctagccact gggacatat tgggtcttct 1150
 tctagctcc tgtctctctc tcatgcctt gctgggtatg ggcctgttag 1200
 ggggaaggct attgctgta gaggggcact gactttctaa tgggtcttacc 1250
 caaggtgaat gttggagaca cagtccgat gctgccaag tccgggcag 1300
 ccttaactat ccaggagatc gctgcctgtg ccaggtctc cctgcctggt 1350
 atgcagccc tccatgttt ctggccact tgtctttct cctccgttt 1400
 gcacatccc ttggaactgt tctctgtgag tacatgctgg ggtctccct 1450
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taatatataaa atcttttctaa atctctataaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
			20						25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
			35						40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
			50						55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
			65						70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
			80						85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
			95						100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
			110						115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
			125						130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
			140						145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
			155						160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
			170						175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
			185						190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
			200						205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
			215						220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
			235						240					245

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Irc	245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
Glu Pro Glu Glu Gln	335		

<210> 34
 <211> 35
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct

<400> 34
 tgtctcttgt cccagacttc tgtcc 25

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 35
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct 50

<210> 36
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 36

<210> 35
ttccactcnaa ttaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ttaggtgagc aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ttaggtgagc ggcctggcca ggctcctccct gcctgggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaca ggcagcctct tg 22

<210> 40
<211> 7084
<212> DNA
<213> Homo sapiens

<400> 40
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tgatatttca gttcctgatt gtaaatacct cctaagccctg aagctttctgt 200
tactagccat tctgagcttc agttttcttca tctgcacaaat gggcataata 250
aatctatctc ttgcacacac aagggtattgt tattccttca aaaaaaaacc 300

aatccccag aagctacaa ttttggcctt agccaaaatt ctgttcattt 350
 caacgttgtt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
 gacataaaca caacacagaa cattgcagaa attttttaaaa caatggaaaa 450
 taacactatt totttggaaa gtgaagcaaa cttaaaactca gataaagaaa 500
 atataaccac ctcaaatctc aaggcgagtc attccctctc ttggaatcta 550
 cccaaacaac gccacgggaat aacagatttc tccagtaact catcagcaga 600
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 gatgaagatc ttttgcccat ctacgcacat cccaatgcta cactgctct 750
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 acctgtatto tagtaagtta taattttcta gatcagcaca cacatgata 1900
 gccaactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
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<210> 41
 <211> 334
 <212> PRT
 <213> Homo sapiens

<400> 41
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 Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
 20 25 30
 Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
 35 40 45
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
 50 55 60
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
 65 70 75
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
 80 85 90
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
 95 100 105
 Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
 110 115 120
 Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
 125 130 135
 Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
 140 145 150
 Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
 155 160 165
 Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
 170 175 180
 Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
 185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
His	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<110> 42
 <111> 1594
 <112> DNA
 <113> Homo sapiens

<400> 41
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 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
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 caagatctg tcaagagtaa gaggaacag atagagtgtc cttggtaata 900
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 gaaaaaaaa aaactacta accactgcaa gctcttctca aattttagtt 1050
 caattggcat tgcctgtttt ttgaaactga aattacatga gtttcatttt 1100
 ttctttgcac ttataggggt tagattttctg aaagcagcat gaatatatca 1150
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 cttctttttt cctttaagta agctctttat ccatcttatg gtggagcaat 1250
 cttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaaata 1300
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 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
 tgtgtaggtg ctgaatctg taaggagttt aggttgtatg aattctacaa 1550
 cctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 41
 <211> 263
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
 1 5 10 15
 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
 20 25 30
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
 35 40 45
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

	40		55		60									
Ser	Ile	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65						70					75
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80						85					90
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95						100					105
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110						115					120
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125						130					135
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140						145					150
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155						160					165
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170						175					180
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185						190					195
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200						205					210
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215						220					225
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala
			230						235					240
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile
			245						250					255
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu							
			260											

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<21> 21
<21> DNA
<21> Artificial

<22> Artificial sequence
<22> 1-20
<22> Synthetic construct.

<400> 45
gaaagatggt atctgatgcc 20

<21> 46
<21> 26
<21> DNA
<21> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
cagatctccc tcttcagtc tgcagc 26

<21> 47
<21> 28
<21> DNA
<21> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
ctctcgaac cacataagtt tgaggcag 28

<21> 48
<21> 15
<21> DNA
<21> Artificial

<220>
<221> Artificial sequence
<222> 1-15
<223> Synthetic construct.

<400> 48
caagattccc tccacagaaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<401> 49
ggagaggaga ggggaggag agagagccc agagagccc agggcaccac 50

26

ggggagggg ggggagggg ggggagggg ggggagggg 1650
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 ggggagggg ggggagggg ggggagggg ggggagggg 1960

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
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 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
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 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
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 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
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 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
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 Ser Gln Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Gln Gln Ala
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Leu	Arg	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
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Ala	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
				185					190					195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
				215					220					225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230					235					240
Gln	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245					250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
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Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
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 <212> DNA
 <213> Homo sapiens

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 <212> PRT
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Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly 80 85 90		
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala 95 100 105		
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val 110 115 120		
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val 125 130 135		
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile 140 145 150		
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro 155 160 165		
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Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly 230 235 240		
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Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly 305 310 315		
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Lys Pro Gly Cys Gln Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly 335 340 345		

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Asp	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly
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Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser
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Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser
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Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg
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 <213> Homo sapiens

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 <211> 250
 <212> FRT
 <213> Homo sapiens

400-54

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Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
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Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
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Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
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Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
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Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
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Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
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Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
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Val	Thr	Gln	Gly	Gln	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
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Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
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Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
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Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
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<212> 1NA
<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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<210> 58
 <211> 1115

<212> PBT
 <213> Homo sapiens

<400> 58

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Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
				35					40					45
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
				50					55					60
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
				65					70					75
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
				80					85					90
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln
				95					100					105
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala
				110					115					120
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln
				125					130					135
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys
				140					145					150
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val
				155					160					165
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met
				170					175					180
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu
				185					190					195
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val
				200					205					210
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr
				215					220					225
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile
				230					235					240
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser
				245					250					255
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser
				260					265					270

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Gln Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg			

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575										585				
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp
590										600				
Arg	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile
605										615				
Arg	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg
620										630				
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys
635										645				
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile
650										660				
Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly
665										675				
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu
680										690				
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr
695										705				
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr
710										720				
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met
725										735				
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr
740										750				
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys
755										765				
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His
770										780				
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn
785										795				
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr
800										810				
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro
815										825				
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg
830										840				
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro
845										855				

Pro	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile			
				860					865					870			
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln			
				875					880					885			
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro			
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Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His			
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Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala			
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Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala			
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Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Gln			
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Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His			
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Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly			
				980					985					990			
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro			
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Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys			
				1010					1015					1020			
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg			
				1025					1030					1035			
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro			
				1040					1045					1050			
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu			
				1055					1060					1065			
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp			
				1070					1075					1080			
Cys	Pro	Gln	His	Ile	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly			
				1085					1090					1095			
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr			
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Pro	Pro	Leu	Thr	Ile													
				1115													

<210> 59
 <211> 29
 <212> INA
 <213> Artificial

<122>
<122> Artificial sequence
<122> 1-25
<123> Synthetic construct.

<400> 59
ggaagacac gacgtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<120>
<121> Artificial sequence
<122> 1-24
<123> Synthetic construct.

<400> 60
gacacgtag cctgtcgtg gacg 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<120>
<121> Artificial sequence
<122> 1-42
<123> Synthetic construct.

<400> 61
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<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<2100>
<211> unsure
<212> 676
<213> unknown base

<400> 62
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 cacatgaaa a 1661

<210> 68
 <211> 460
 <212> 1PT
 <213> Homo sapiens

0220 - unsure
 0221 - 196, 386
 0222 - unknown amino acid

0400 - 63

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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Gln	Gln	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

	275	285	295
Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro	275	280	285
Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu	290	295	300
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly	305	310	315
Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu	320	325	330
Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg	335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp	350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu	380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val	410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser	425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val	440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala	455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro	470	475	480
Thr Phe Thr Gln Trp Leu Cys	485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-21

<223> Synthetic construct.

<411> 14

<210> 1-25

<211> 65

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

atcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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ggcccagcaa gcttgataag catgaagctc ttatcttttg tggtgtgtgt 150
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<210> 68
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 68
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 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

11	Met	Trp	Val	Trp	Gly	His	Asp	Val	Glu	Ala	Tyr	Lys	Leu	Leu	
			41						71				75		
	Tys	Glu	Tys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				63						85				90	
	Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95						100				105	
	Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110						115				120	
	Ala	Tyr	Thr	Glu	Glu	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125						130				135	
	Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala
				140						145				150	
	Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
				155						160				165	
	Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
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<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
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 tccctttgca tcccaacccc tccgggtttt gcttcttctt ggggaacccc 200
 tgcgggggag atggccgctt tgatgcggag caaggattcg tctgctgcc 250
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 tggtcaggcc gccaatcatt ctccgggcct gtaccaagga ctggcattcg 400
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<210> 70
 <211> 259
 <212> FRT
 <213> Homo sapiens

<400> 70
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 20 25 30
 Ser Arg Ala Lys Leu Asp Ser Ile Lys Ser Ser Leu Gly Gly Glu
 35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 75 100
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 90 115 140
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 105 130 155 180
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 120 145 170 195
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 135 160 185 210
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 150 175 200 225
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 165 190 215 240
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 180 205 230 255
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 195 220 245 270
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 210 235 260 285
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 225 250 275 300
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 240 265 290 315
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 255 280 305 330
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 270 295 320 345
 Cys Gln Lys Ile

<E10> 71
 <E11> 1809
 <E12> DNA
 <E13> Homo sapiens

<400> 71
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 attccttata acctcttatg tctcaatcag gaaggtatg :catttatt 200

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 aaataacttg atgtgtttta aggccttggg caaaaattct gtattgttga 350
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Ser Ser Gln Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys	230	235	240
Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala	245	250	255
Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser	260	265	270
Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser	275	280	285
Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln	290	295	300
Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn	305	310	315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr	320	325	330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg	335	340	345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp	350	355	360
Leu Ile Arg			

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<210>
 <211> Artificial sequence
 <212> 1-26
 <213> Synthetic construct.

<400> 73
 atttcattggc aaatatitcc ctcccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<210>
 <211> Artificial sequence
 <212> 1-22
 <213> Synthetic construct.

<400> 74
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<210> 75
 <211> 50

<210> DNA
<211> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac ccgtcccttg ctcaggattt ggagagcttg caccacccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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 caataaagtc cccatctgat tttaaaaaa aaaaaaaaa 1989

<110> 77
 <111> 341
 <112> PRT
 <113> Homo sapiens

<400> 77
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 Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
 35 40 45
 Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
 50 55 60
 Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys His Val Leu Ala Val
 65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr	Tyr Val Asn Arg	Gly His
80	85	90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His		
95	100	105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg		
110	115	120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro		
125	130	135
Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu		
140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp		
155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu		
170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala		
185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser		
200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val		
215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln		
230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu		
245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu		
260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn		
275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg		
290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu		
305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp		
320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys		
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<210> 78
 <211> 2243
 <212> ENA
 <213> Homo sapiens

<400> 7A

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 <211> 475
 <212> PRT
 <213> Homo sapiens

<400> 79
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 Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
 35 40 45
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
 50 55 60
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
 65 70 75
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
 80 85 90
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
 95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395		400		405
Leu Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser					
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Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu					
	425		430		435
Thr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly					
	440		445		450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser					
	455		460		465
Ala Cys Ser Thr Leu Leu Val His Leu Ile					
	470		475		

<210> 30
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> #0
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<210> 31
 <211> 33
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1-23
 <223> Synthetic construct.

<400> A1
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<210> 32
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 62
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<210> 33
 <211> 1-44

212 - DNA
213 - H. m. sapiens

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tctctgctct cgtcccccato ctctctcagcc tggctggcctc ccaggactgg 150
aaggctgaac gcagccaaga ccccttcagag aaatgcctgc aggatcctga 200
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<110> 84
 <111> 567
 <112> FRT
 <113> Homo sapiens

<400> 84
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 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Gln Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala	Leu Arg Ile	Gln Gln	Lys Gly His	Ser Pro	Glu	
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Asp Ile Tyr Gln	Met Ala Leu	Asn Gln	Ala Leu Lys	Asp Leu	Lys	
	185		190		195	
Ala Leu Gly Cys	Arg Lys Ala	Met Lys	Lys Phe	Glu Arg	His Thr	
	200		205		210	
Leu Leu Glu Tyr	Leu Leu Gly	Glu Gly	Asn Leu	Ser Arg	Pro Ala	
	215		220		225	
Val Gln Leu Leu	Gly Asp Val	Met Ser	Glu Asp	Gly Phe	Phe Tyr	
	230		235		240	
Leu Ser Phe Ala	Glu Ala Leu	Arg Ala	His Ser	Cys Leu	Ser Asp	
	245		250		255	
Arg Leu Gln Tyr	Ser Arg Ile	Val Gly	Gly Trp	Asp Leu	Leu Pro	
	260		265		270	
Arg Ala Leu Leu	Ser Ser Leu	Ser Gly	Leu Val	Leu Leu	Asn Ala	
	275		280		285	
Pro Val Val Ala	Met Thr Gln	Gly Pro	His Asp	Val His	Val Gln	
	290		295		300	
Ile Glu Thr Ser	Pro Pro Ala	Arg Asn	Leu Lys	Val Leu	Lys Ala	
	305		310		315	
Asp Val Val Leu	Leu Thr Ala	Ser Gly	Pro Ala	Val Lys	Arg Ile	
	320		325		330	
Thr Phe Ser Pro	Pro Leu Pro	Arg His	Met Gln	Glu Ala	Leu Arg	
	335		340		345	
Arg Leu His Tyr	Val Pro Ala	Thr Lys	Val Phe	Leu Ser	Phe Arg	
	350		355		360	
Arg Pro Phe Trp	Arg Glu Glu	His Ile	Glu Gly	Gly His	Ser Asn	
	365		370		375	
Thr Asp Arg Pro	Ser Arg Met	Ile Phe	Tyr Pro	Pro Pro	Arg Glu	
	380		385		390	
Gly Ala Leu Leu	Leu Ala Ser	Tyr Thr	Trp Ser	Asp Ala	Ala Ala	
	395		400		405	
Ala Phe Ala Gly	Leu Ser Arg	Glu Glu	Ala Leu	Arg Leu	Ala Leu	
	410		415		420	
Asp Asp Val Ala	Ala Leu His	Gly Pro	Val Val	Arg Gln	Leu Trp	
	425		430		435	
Asp Gly Thr Gly	Val Val Lys	Arg Trp	Ala Glu	Asp Gln	His Ser	
	440		445		450	
Gln Gly Gly Phe	Val Val Gln	Ile Pro	Ala Leu	Trp Gln	Thr Glu	

455	460	465
Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Pro Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Glu Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
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545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
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 tattacatat aaaaaa 3316

<210> 86
 <211> 734
 <212> FFT
 <213> Homo sapiens

<400> 86
 Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
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 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
 20 25 30

Pro	Pro	His	Pro	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	45	
Ala	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	50
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	65
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	80
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	95
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	110
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	125
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	140
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	155
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	170
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	185
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	200
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	215
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	230
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	245
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	260
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	275
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	290
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	305
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr	

His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val	320	325	330
335	340	345	
Glu His Ala Tyr Glu Phe Thr Pro Asp Asp Val Ala Ile Ser Tyr	350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val	365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg	380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro	395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn	410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val	425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp	440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu	455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser	470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val	485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe	500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu	515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr	530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn	545	550	555
Val Ile Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala	560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp	575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile	590	595	600
Phe Lys Leu Ala Gln Gly Gln Tyr Ile Ala Pro Glu Lys Ile Glu	605	610	615

Asp	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Ile	Val	His
									625					630
Gly	Ala	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
									640					645
Thr	Asp	Val	Leu	Ile	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
									655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
									670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
									685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
									700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
									715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
									730					735

His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 cccctcatca agccctttgg gctcggaag aagcggagct ggtaccttac 200
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Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
65 70 75
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Arg Pro Arg Arg
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Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
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Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
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Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
125 130 135

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Met	Val	Ala	Pro	Gly	Arg	Val	Leu	Ile	Lys	Thr	Val	Lys	Asp	Glu	
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Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu	Arg	Ser	
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Ser	Lys	Ser	Pro	Ala	Leu	Ser	Ser	Trp	Gly	Asp	Pro	Val	Leu	Leu	
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Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His	
					245				250					255	
Trp	Ala	Asp	Thr	Glu	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Phe	Cys	Ser	
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Lys	Val	Glu	Gly	Tyr	Gly	Ser	Val	Cys	Ser	Cys	Lys	Asp	Pro	Thr	
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Pro	Ile	Glu	Phe	Ser	Pro	Asp	Pro	Leu	Pro	Asp	Asn	Lys	Val	Leu	
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Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val	Ser	Pro	
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425	430	435
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Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
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Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
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Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
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Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
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Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
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Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
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Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
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Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
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Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
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Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
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<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

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<222> 1-32
<223> Synthetic construct.

<400> 30
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<210> 31
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<223> Synthetic construct.

<400> 31
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<223> Synthetic construct.

<400> 32
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<223> Synthetic construct.

<400> 33
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<210> 34
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<211> 307

<212> PRT

<213> Homo sapiens

<400> 95

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Val	Gly	Cys	Tyr	Val	Ala	Gly	Ile	Ile	Pro	Leu	Ala	Val	Asn	Phe
				20					25					30

Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu
				35					40					45

Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His
				50					55					60

Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser
				65					70					75

Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser
				80					85					90

Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His
				95					100					105

Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu
				110					115					120

Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp
				125					130					135

Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu
				140					145					150

Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala
				155					160					165

Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val
				170					175					180

Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser
				185					190					195

Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His
				200					205					210

Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr
				215					220					225

Tyr Leu Gly Leu Ser Lys Ser Ser Lys Gln Ala Leu Ser Gln Val

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245	250	255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly		
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg		
275	280	285
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290	295	300
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305		

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 <213> Artificial

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 <223> Synthetic construct.

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<210> 37
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 <212> DNA
 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct.

<400> 37
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121. + RNA
 121. + Homo sapiens

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<211> 401

<212> FRT

<213> Homo sapiens

<400> 100

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			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
			230						235					240

Glu	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Glu	Glu	Thr	245	250	255
Asn	Glu	Ile	Gln	Val	Val	Asn	Glu	Glu	Pro	Gln	Arg	Asp	Arg	Leu	260	265	270
Ile	Gln	Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val	275	280	285
Gly	Gly	Arg	Gly	Phe	Gly	Gly	Ala	Gly	Glu	Leu	Gly	Gln	Thr	Pro	290	295	300
Gln	Val	Gln	Ala	Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met	305	310	315
Glu	Gly	Pro	Glu	Arg	Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu	320	325	330
Glu	Glu	Gln	Glu	Ala	Ala	Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu	335	340	345
Arg	Gly	Glu	Asp	Asp	Tyr	Asn	Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser	350	355	360
Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile	365	370	375
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu	380	385	390
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<210> 101

<211> 3671

<212> DNA

<213> Homo sapiens

<400> 101

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tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccca 200
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gatccccggc tctaccgata tcaggttgac cctctacca ccaccatgca 400
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 211> 1089
 212> PRT
 213> Homo sapiens

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 Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
 20 25 30
 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Glu Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Trp Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

	205	205	210
Leu Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
215	220	225	
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
230	235	240	
Gly Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
245	250	255	
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
260	265	270	
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
275	280	285	
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
290	295	300	
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
305	310	315	
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
320	325	330	
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
335	340	345	
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
350	355	360	
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
365	370	375	
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
380	385	390	
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
395	400	405	
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
410	415	420	
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
425	430	435	
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
440	445	450	
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
455	460	465	
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
470	475	480	
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
485	490	495	

Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu
				515					515					516
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe
				518					520					525
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala
				530					535					540
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe
				545					550					555
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala
				555					555					570
Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val
				575					580					585
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu
				590					595					600
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg
				605					610					615
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu
				620					625					630
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr
				635					640					645
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met
				650					655					660
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala
				665					670					675
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg
				680					685					690
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg
				695					700					705
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala
				710					715					720
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu
				725					730					735
Val	Ser	Gly	Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu
				740					745					750
Ala	Ala	Ser	Gly	Leu	Ala	Leu	Leu	Leu	Trp	Lys	Pro	Val	Thr	Val
				755					760					765
Leu	Val	Lys	Ala	Gly	Ala	Gly	Ala	Pro	Arg	Thr	Arg	Thr	Val	Leu
				770					775					780
Thr	Pro	Phe	Ser	Gly	Pro	Pro	Thr	Ser	Glu	Ala	Asp	Leu	Asp	Tyr

805	890	975
Val Val Ile Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly		
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala		
815	820	825
Thr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu		
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile		
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu		
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe		
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr		
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile		
905	910	915
His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser		
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala		
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp		
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro		
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu		
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe		
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu		
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg		
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe		
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly		
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Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe		
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Att Ala Leu Thr Ile Ala Ser Ala Arg
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<211> 1743
<212> DNA
<213> Homo sapiens

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ttcaaggagt taaagtiact tacaatgtgc aqtatttcat cacaaattgg 200
cccaccagag gtggcaactg ctacagatga gaagtcacatt tctgtttgct 250
tgacagctcc agagaagtgg aagagaaaac cagaagacct tctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaac agaacgttgt ccagtggtg gaccaaccac acgctggtgc 400
tcacctgctt ggagccgaac actcttact gcgtacacgt ggagtcttcc 450
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gaatttgaaa gatcaatcat cagagttcaa ggctaaaac atctttctgt 550
atgttttgcg catatctatt accgtgttcc tttttctgt gatgggctat 600
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gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
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 <211> 442
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Gln Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

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Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
				215					220					225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
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Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
				320					325					330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
				335					340					345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
				350					355					360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
				365					370					375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
				380					385					390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
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Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
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Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
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Leu	Tyr	Val	Gln	Met	Glu	Asn									
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<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cprtgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
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<222> 1-18
<223> Synthetic construct.

<400> 106
cactgtgccg ggaacttg 18

<210> 107
<211> 13
<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 107
cprtgccaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
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<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<122> 1-51

<12> Synthetic construct.

<400> 109

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c 51

<310> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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gtctctgggg ggccagatc atggggggcc acgaggtgac cccccactcc 200

aggccctaca tggatccct ggcctctggg gcccacacac actgaggagg 250

cttctgtatg agagcccgct gggctgtctc agcccccac tgcctcagcc 300

acagagacat cggcactggc ctggtggtgc tgggcgcaca cgtcttgagt 350

actggggagc ccaaccagca agtgtttggc atcgtatctc tcaccaagca 400

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gggtttctgc tgggcagact ccggagggcc cctggtgtgc aggaacgggg 750

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cccgactgt acacgcagg gtccgccttt ctgacctgga tctgggacgt 850

ggttcggggg agcagtcacc agcccgggcc cctgcttggg accaaccaggc 900

ccccaggaga acccgctga gccacaaact tgggcatgc aaatgagatg 950

gcccctccac gcttgaatg ttccgtggct gggcccacg ggaagcctga 1000

tgttcagagt tgggtggga cgggcagggc tgggcacac ccattccac 1050

tggggggg agacacaa ccattcaaat gttaaataa aaaaaaaa 1100

pass 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
			35						40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pr His Pr Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<210>
<211> Artificial Sequence
<212> 1-24
<213> Synthetic construct.

<400> 112
gagctctctca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<210>
<211> Artificial Sequence
<212> 1-23
<213> Synthetic construct.

<400> 113
ggaaggaa acgagggcgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<210>
<211> Artificial Sequence
<212> 1-44
<213> Synthetic construct.

<400> 114
agacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> RNA
<213> Homo sapiens

<400> 115
gagctareca gggggctggg gtgcagcaag atccggcgcg actccggagc 50
actgaagcct gaagcctgtc ccgggcagg catgagcgcg tacctctctg 100
cggctgtagc actggacagc atagcagcc ccggcctcct gctcaaggac 150
tatgtacagc gtggggcttg cccagagag accacatcc ctgggaagac 200

tgcacgtg aggggagaa aacatcat cgggaaga acatctt 251
 aactggccag gagaggaagc aacatcatc tggctgacg agaatggag 300
 aagtgtgagg cggcagcaaa ggaatccgc ggggagacc tcaatcaca 350
 tgtcaagcc cggcacctgg acttgcttc cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggagaagc gagtggacat tctaatcaac 450
 aacgggggtg tgatgcagtg ccccaactgg aacacgagc acggtctga 500
 gatgcagttt ggctttaacc acctgggtca cttctcttg aaaaacttgc 550
 tgcaggcaaa gctgaaagcc tcagccctt cgggacat caacctctg 600
 tccctggccc atgttgcgtg gacatagac tttagagact tgaactggca 650
 gacgaggaag tataacacca aagccgccta ctgcagagc aagctggca 700
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 gctgtccg gaggttcca aggtgctcc tgaagagcat gggcaagtgc 1450
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 gctctcttg accttggct tcttcagag tgapatgct agaataactg 1550
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 tctctgca aggtcttc ctgaggtt cctatggag acatcaaca 1650

gagagcaggt gcaagttatc tccagattc aggcctgca aggcagga: 170
 tgggaacccc accagatatt gctacaggaac ctgggattac ctggaattc: 1710
 cacccttcta tcaatttcca tctagtcca caactgagac tctcgaattt 1800
 gctcattt 1808

<U10> 116
 <U11> 331
 <U12> PRT
 <U13> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	
				230					235					240	
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	
				245					250					255	
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	
				260					265					270	
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	
				275					280					285	
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	
				290					295					300	
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	
				305					310					315	
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	
				320					325					330	

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
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 ctggcggtgc tggcgctcg gacaggagac ccagaaaggg ctggcgctcg 100
 gggcgacacg ttctggcggc tgaccagcgt ggcggcgggc ctggcgcccg 150
 agcgcgggct gctggggctg ctgaggcggt acctggcggg ggaggaggcg 200
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcattg 250
 ggattcaaca acccctgtgg ctaacctct gattgcattt actctcatca 300
 aacgctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggetat gagaaggtgg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aadggccctg atcgggctgc 450
 aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
 agagtcactg gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaaat tctcaaggtg gcttatgaca 600
 tgggggalla ttacatgccc attccatggc tggaggagcc tgtcagcttc 650
 ttcggatcat attctccaca gtggaacaca cagatcacc caactctaca 700

agatgacttg gatcaattga cctttgctta tttccgggca ggaattgttt 710
 cgtatgacct cagcctctct cgggagtttc ttctctacac cccagatatt 800
 aagaggtatg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 ccccaaccac gtggtagctc aggtgtctat ccagaggccc aatatcccc 900
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctggatttc 950
 cagcccactc tctaccagat ccttagcctc taactgttct atgagacca 1000
 ttccaacgca tactgtctgc tccagcccat ccggaaggag gtcaccacc 1050
 tggagcccta cattgtctc tactatgact tggcagtgca ctccagggt 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtgc 1150
 atcaggggag aagcagttac aagtggagta ccgcaccagc aaaagtgcct 1200
 ggtgaagga cactgttgac ccaaaactgg tgaccccaa ccacccgatt 1250
 gctgcctca caggccttga tgtccggcct ccttatgcag agtatctga 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgacatg 1350
 ctacgtcacc aagcagcccc ctctacagaa tgaagtccgg aaaccgagtt 1400
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 ctccatctat gcaacctca gctgtcctgt ggtaggaat gcagcactgt 1500
 tttggtggaa cctgcacagg agtggtgaag gggacagtga cacacttcac 1550
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 acatgagtat ggacaggaat ccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctgggtg agtccctgtg ctttccagag 1700
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gcctgtcag ctttgtctgt gcctcgcaaa ccagaggcaa 1800
 gggagaggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
 agccacggaa gtcagagtag gatgcacagt acaagggagg ggggagt gga 1900
 ggccctgagag ggaagtctct ggagttcaga taactctctgt tgggaacagg 1950
 acatctcaac agtctcaggt ccgatcagt ggtcttttgg cactttgaac 2000
 cttgaaccac gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
 tagcctcaat ccagaaact taagatttc tcccaactgc cttctctac 2100
 agcccaagga ggaattctct ccttcacaa aatatccc agatcaactg 2150

tcattatatt aaggattttt tttaattga aaacaaattt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

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Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Glu Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	
				245					250					255	
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	
				260					265					270	
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	
				275					280					285	
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	
				290					295					300	
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	
				305					310					315	
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	
				320					325					330	
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	
				335					340					345	
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	
				350					355					360	
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	
				365					370					375	
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	
				380					385					390	
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	
				395					400					405	
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	
				410					415					420	
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	
				425					430					435	
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	
				440					445					450	
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	
				455					460					465	
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	
				470					475					480	
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	
				485					490					495	
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	
				500					505					510	
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	
				515					520					525	
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser	

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

ctttacatga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ctttcaatga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctttcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

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tcccacctt aggaagccac cagaactccac agtgtggggc caatcaggtc 100

gaatggccc tgcaggttg agccagagc gctggctgag ggacagagcc 150

ggagagccc ggaacccag taaccagcac ggggacgccc caggatcccc 200

ggagggaact agagagat ggaatacgc gggcattct cctacatctg 250
 gctcaagttt taattatca tctattcac cgtgtttctg ctgattggg 300
 cctgggtcct atctatgggc atctatgcag aggttgagcg gcagaaatat 350
 aasacccttg aaagtgcctt cctggctcca gccatcctcc tctctctct 400
 gggcgtcgtc atgttcatgg tctcttcat tgggtgctg ggttcctcc 450
 gtgacaacct gtacattctc caagattcca tgtacatctt tgggatctgc 500
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 gacattgac ttctgaaag acaacattcg aagagggaatt gagaactact 600
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 tcttgagcc tactttttt ttacgtgatt ttctataaat tcattttttt 1650

ctacacatca caggacttca tgcctacaca aacatgatat ttcacagcat 1732

atcttattc tgcctctccc ccaaccagtt tcttaatcaa acaataaaaa 1750

catgttttgt tttgttttta aaaaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

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Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
		20							25					30

Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
			35						40					45

Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50						55				60

Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75

Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
			80							85				90

Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
			95						100					105

Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
			110						115					120

Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
			125						130					135

Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
			140						145					150

Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
			155						160					165

Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
			170						175					180

Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
			185						190					195

Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
			200						205					210

Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
			215						220					225

Trp	Phe	Met	Asp	Asp	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
			245						250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
			260						265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
			275						280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
			290											

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct.

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<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
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<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-50
 <223> Synthetic construct.

<400> 126
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<210> 127
 <211> 1636
 <212> RNA
 <213> Homo sapiens

420 - 127

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Ser Ile Asp Arg Leu Gln Phe Asp Leu Leu Tyr Pro Ala Ile Lys
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
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Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
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Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
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Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
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Pro Val Ser Gln

*210-129

*211-2212

*212-INA

*213-Homo sapiens

4000-129

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<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
110 115 120

Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
125 130 135

Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
140 145 150

Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
155 160 165

Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
170 175 180

Ile Ala Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
185 190 195

Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
200 205 210

Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
215 220 225

Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
230 235 240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
245 250 255

Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
260 265 270

Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
275 280 285

Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
290 295 300

Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
305 310 315

Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
320 325 330

Ser Phe Leu Met Ser
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<210> 131

<211> 2476

<212> PNA

<213> Homo sapiens

<400> 131

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<210> 132
 <211> 535
 <212> PRT
 <213> Homo sapiens

<400> 132
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 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

Asn	Ser	Ile	Ile	Tyr	Tyr	Ile	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
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Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				98					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

365	370	375
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380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
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Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
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530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

*400> 134

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Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25					30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40					45

Ile	Ser	Lys	Gly	Leu	Trp	Met	Gln	Tyr	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
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Asp Ile Gln Ala Ala Gln Ala Met Met 80	Val Thr Ser Ser Ala Ile 85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val 95	Val Gly Met Arg Cys Thr 100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys 110	Asp Arg Val Ala Val Ala 115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly 125	Leu Leu Gly Phe Ile Pro 130	135
Val Ala Trp Asn Leu His Gly Ile Leu 140	Arg Asp Phe Tyr Ser Pro 145	150
Leu Val Pro Asp Ser Met Lys Phe Glu 155	Ile Gly Glu Ala Leu Tyr 160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser 170	Leu Ile Ala Gly Ile Ile 175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg 185	Asn Arg Ser Asn Tyr Tyr 190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala 200	Thr Arg Ser Ser Pro Arg 205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser 215	Glu Phe Asn Ser Tyr Ser 220	225
Leu Thr Gly Tyr Val 230		

<110> 135

<111> 610

<112> DNA

<113> Homo sapiens

<400> 135

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agccatcgtg tccctgagcg agaccgcgca atgtgtctcc ccttcacact 250
tttggacctg ctttagctct tctgtctctt attcctcttg cctcacaacc 300
cattctcttg tgaacctgaa gttccagatg gttcattccc agtgcaccta 350

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ctctccatc tccagtaaat ctgagagcag agagcgtttt ccccgagaa 400
 acatagaaaag aaaatcraact ctcaataagc catctcagaa acataggcta 450
 aggtaatatg tctaccagta cagaagccctg aggaattttac aaattgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
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<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
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 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gtgggggaaa gttctcaggac cccctgcagc actgtttgcta tgatgatgac 200
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<210> 138
<211> 110
<212> PRT
<213> Homo sapiens

<400> 138
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Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35 40 45
Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50 55 60
Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65 70 75
Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
80 85 90
Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95 100 105
Cys Arg Ser Val Ser
110

<210> 139
<211> 2044
<212> DNA
<213> Homo sapiens

<400> 139

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0110: 140
 0111: 311
 0112: PRT
 0113: Homo sapiens

0400: 140
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
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 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 ccttctccga ccccgctcta gcagcagacc tctgggggtc tgtgggttga 200
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 agatactc ccccgagc ctggacac tcttggag cacaagct 450

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 aacgcctaca ctgtccgctt gtcactccc ccnagcctgt gacggagcca 550
 cagcaatgct gtcccaagtg tctggaacct cacactccct ctggactccg 600
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 aatctctcag tgcacatgag ctgttccctt ccrgcctgcc caaccagtgt 700
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 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacattgtg 850
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 aagaacttcc gaaagaggca cagcacttcc gaactctcgc tggcccccac 1550
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<210> 142
 <211> 451
 <212> FRT
 <213> Homo sapiens
 <400> 142

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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	
				20					25					30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	
				35					40					45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	
				50					55					60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	
				65					70					75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	
				80					85					90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	
				95					100					105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	
				110					115					120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
				125					130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Gln Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450

Thr

<.10> 143
 <.11> 693
 <.12> DNA
 <.13> Homo sapiens

<400> 143
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 cttgcggaaa atgctgatct cagtgcgaat gctggggcgca gggcttgccg 150
 tgggtaacgc cctcctcgtt atcgtgaccc cgggagagcg ggggaagcag 200
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 caattgggt tggggcagg aatcagaggc agcattctc cttcgtgggc 450

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<10> 144
 <11> 93
 <12> FST
 <13> Homo sapiens

<10> 144
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 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<10> 145
 <11> 1883
 <12> DNA
 <13> Homo sapiens

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 atgtctggga cccctccaaag gacagcagca ccaccttctg gactacatgg 200
 aacgccgaat agctgcctta gaggaacggc tggcccagtg ccaggacag 250
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 atgtctggga gtggcagaga aggaacggga ggaactcaga actgagacac 350
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450 tttttttttt aaacagatctt tttttttt aaattttt aaattttt 450
 500 tttttttt gggacaaaa gaaaggaat aaagaaat aaataagata 500
 550 tttttttt aa ctgttgctac acaatcttc aagtgaatc aatgaagatt 550
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 1800 aaagggaat tctcccaatt gttttgtat gcaaatctt gattaaaa 1800
 1850 tttttttt aaacaaaa aaacaaaa aaacaaaa aaacaaaa 1850

146
 406
 187
 Ham sapiens

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5					10					15
Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Ile	Arg	Ala	Val	Gly	Leu	Ile	Pro	Phe	Tyr	Gly	Leu	Thr	Ala
				260					270					275
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala
				275					280					285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys
				290					295					300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro
				305					310					315
Gly	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr
				320					325					330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile
				335					340					345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala
				350					355					360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu
				365					370					375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly
				380					385					390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu
				395					400					405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctctctt tctctctaat ccctccgtca cctctctctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccctggctct catgctcagt 200
 ttgggttctga gtctctctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttgggtggg ggaggacgca gcattctctt 300
 gtttctgttc tcttaagacc aatgcadagg ccctggaagt gcggttcttc 350
 agggggcagt tctctagagt ggtccacctc tacagggaag ggaaggacca 400
 gccatttatg cagatccac aatatcaagg caggacaaaa ctggtgaagg 450
 attctatttc agagcagcg atctctctga ggtgcaaaa ccttactgtg 500

ttatattg aattatgt atcaaat attcaat attatcaa 550
 aaacacac tggagttac aggtatgaa actggjctca gttctctca 600
 tttctctca tggatattgt gataaaaca tccagatact ctgtcactcc 650
 tccggtgat tcccccggcc aacagcgaag tggaaaggtc cacaaggaca 700
 gaatttgtcc acaaatccca ggaacaacag agacatccat ggctgtttg 750
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 agagataac tttttgagc ctatategtc gcacctggt accaaagtac 900
 tgggaatact ctgtgtggc ctattttta gcaattgttg actgaagatt 950
 ttctctcca aattccagt gaaaatcag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagagc ccggaacac gcagtggag 1050
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 aaaactgtaa cccatagaaa agctccccc gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tggtggttc tcagagtttc caagcaggg 1200
 aacattactt ggaggtggc ggaggacac ataaaaggtg gcgctggga 1250
 gtgtgcggg atgatgtga caggaggaag gactaagtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttacc agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggctc tctggacta tgagtgtgg accatctctc tctcaacat 1450
 aatgaccag tcccttattt atacctgac atgtcggttt gaaggcttat 1500
 tgaggcccta cattgagtat ccgtctata atgagcaaaa tggaaactcc 1550
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 aagggcctct gcaatcccag agacaagcaa cagtgaagtc tctcacagg 1650
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 atggaatca gctgtcatgg ctgacctgag ctgggaagga agaaggctga 1850
 cattacatt agtttctct cactcatct ggttaagtga tcttcaata 1900
 caacttcca gttgaaga tctcaggaat tctcttca caagttgtg 1950

230	235	240
Gly Ile Leu Cys Cys Gly Leu Ile Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Ile Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

210 149

211 24

<212> DNA
<213> Artificial

<214>
<215> Artificial Sequence
<216> 1-24
<217> Synthetic construct.

<218> 149
gcctagtgaca cctctacagc gacg 24

<219> 150
<220> 23
<221> DNA
<222> Artificial

<223>
<224> Artificial Sequence
<225> 1-23
<226> Synthetic construct.

<227> 150
tggctgacc cagtgcctgac acc 23

<228> 151
<229> 45
<230> DNA
<231> Artificial

<232>
<233> Artificial Sequence
<234> 1-45
<235> Synthetic construct.

<236> 151
gcagatgaca cagtatcaag gcaggacaaa actggtgaag gattc 45

<237> 152
<238> 2194
<239> DNA
<240> Homo sapiens

<400> 152
gccatggtgc gcccggtggc ggtggggggc gcggttgccg aggccttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatgga ggagccgaga gcgccatgag gaggctgccg agcctgggcg 150
gctcgccct gttgtgctgc gcgcgcgcgc ccgcgcgcgt cgcctcagcc 200
gctcgggcgg ggaatgtcac cagtgggcgc ggggcgcgcg ggcadgtgga 250
caggtgcgcg ggccccgggt tgcggggcga ggcagccac ccttcctcta 300
tgcagcggg tcccagggc cagggccgga ggcgcgggc tgcgcgggc 350
acgttaca cgcacctaca tgcgactt ct gcagccact gcgcagagc 400

tttttttttt actttttttt cttttttttt tttttttt ttattttttt 1900
 tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 1950
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<210> 153
 <211> 258
 <212> PET
 <213> Homo sapiens

<400> 153
 Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
 1 5 10 15
 Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
 20 25 30
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
 35 40 45
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
 50 55 60
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
 65 70 75
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
 80 85 90
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
 95 100 105
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
 110 115 120
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
 125 130 135
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
 140 145 150
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
 155 160 165
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

	170		171		172
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn					
	185		190		191
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr					
	200		205		210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys					
	215		220		225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu					
	230		235		240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro					
	245		250		255
Cys Asn Arg					

<210> 151
 <211> 14
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 ...ctgctctg tggttggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 ...gtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 ...gttatatg aggtatcat gtgaacatg aaagaga 38

<I10> 157
 <I11> 689
 <I12> DNA
 <I13> Homo sapiens

<400> 157
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 ctggaacctg agcagcttct tgggcccagg taagtgttg cggtaggcctc 150
 ccgggaaaag ggctttgcca tggagaagga catgaagaac gtctgggggg 200
 tgggtgtgac cctcactcca gaaaacaacc tggggaagct gtctctcag 250
 caagggtgg gagggtgtga ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tggtaggcac caacttcaga gactatgcca tctcttccac tcagctggag 400
 ttgggggacg agcccttcaa cccgtggag ctgtacagtc tgaaggagac 450
 agccagccag gaggccatgg ggctcttccac caagtggagc aggagccctg 500
 gcttctgttc acagtagcag gccagctgc agaaggacct cactgtgtct 550
 cacaagatcc ttctgttgt gtgcgctccc cagtgggat ggcccccaca 600
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 ggcccagca ccagctcaga ataaagcgt tccacagca 689

<I10> 158
 <I11> 163
 <I12> PRT
 <I13> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120
Phe	Thr	Gln	Leu	Gln	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
			155						160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaaatgct gacgatgcag agttccgtga cgggtgcagg aggcctgtgt 150
gtccatgtgc cctgctcctt ctcctacccc tcgcatggct qgatttacc 200
tgcccacgta gttcatggct actgggtccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctggggcagt gtgggaggag 300
actggggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcacc agagatgcca gaagaagtga tggggggaga tacttcttcc 400
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gtgagcaggg gacacccct atgatctct ggatagggac ctccgtgtcc 600
cccctggacc cctccaccac ccgtcctcg gtgctcacc tcattccaca 650
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cagaacttga ccatgactgt ctccaagga gacggcacag tatccacagt 800
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ctgaattgga gaggctgac cctgtgcccc tccagacct caaacgggg 950

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 tttttctctg caggaagana tgggaagtc cagcagcggg cgtgggagat 1200
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 acagacaaat tctc 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
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Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	110	115	120
	125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140	145	150
Tr Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Glu Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Gln	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405

Trp	Ala	Glu	Asp	Ser	Pro	Ile	Asp	Gln	Pro	Pro	Pro	Ala
		410					411					420
Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala
		425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly
		440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg
		455					460					

<211> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
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 ctggaggag gaggatata cagggaacct gtaagtgaag gccatggtgg 150
 tcgataagga ctttcaggag gacaggagcc ccagggaaggt gtccccagt 200
 aaggtgacag cctggggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gaggaggat cgggtgcacc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacaggcc tatgggggca ggaagtcac gtacctgcag 350
 gagctgcaca ggagggaaca ctacatcttt tactgcaaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat ctgatacca 450
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 acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tcagccatg acccttcct 650
 gctcccacc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> FRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

	20		25		30									
Asn	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Ile	Pro	Glu	Asp	Arg	Arg
			35						40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
			50						55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
			65						70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
			80						85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
			95						100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
			110						115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
			125						130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
			140						145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
			155						160					165
Cys	Val	Pro	Glu	His										
			170											

<210> 163

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
tgcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
tctatagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggagacctg gtacgtgaag gccatggtgg tcgataagga ctttcggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgttccttca ccttgaggga ggaggatata acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

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 ctagggtgag aaaccaggat catcaagggg ttgagtgca agctcactc 200
 ctaggcttg gaggcagccc tgttcagaga caggcggcta ctctgtggg 250
 ctacgtcat cgcctccaga tggctctga cagcagccca ctgctcaag 300
 ctacgtaca tagttcact gggtcagcac aacctccaga aggaggagg 350
 ctctgagcag acccggacag caactgagtc cttccccac ccaggcttca 400
 aaacagcct ccccaacaaa gaccaccca atgacatcat gctgggtgaag 450
 atggcatgca cagtctccat cactggggt gtgcagcccc tcaacctctc 500
 ctacgtgtg gtactgtg gcaccagct ctcatttcc ggctggggca 550
 caagtcacg cccacagtta cgcctgcctc acaccttgag atggcccaac 600
 atcaccatca ttgagacca gaagtgtgag aaagctaac ccggcaacat 650
 cacagacac atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
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 aaatatctgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170

<211> 250

<212> FRT

<213> Homo sapiens

<400> 170

Met Arg Ile Leu Ser Leu Ile Leu Leu Ala Thr Gly Leu
 1 5 10 15

<210> 171
 ...tgggaaatga tggg 24

 <211> 172
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 172
 ...tgggaa tgggattct gcag 24

 <210> 173
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 173
 ...tctgtgtct gtaaccag 18

 <210> 174
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
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 <222> 1-24
 <223> Synthetic construct.

 <400> 174
 ...ctgtgatct tgcgggggta ggcg 24

 <210> 175
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 175
 ...ctgtatgca ccaggatttc gggg 25

 <210> 176
 <211> 24
 <212> DNA

<11> Artificial

<111> Artificial Sequence
<112> 1-18

<113> Synthetic construct.

<400> 176

gaggaatga tctgata 18

<110> 177

<111> 50

<112> DNA

<113> Artificial

<110>

<111> Artificial Sequence

<112> 1-50

<113> Synthetic construct.

<400> 177

agggcatgag gattctgag ttaatcctgc ttgctctggc aacagggctt 50

<110> 178

<111> 43

<112> DNA

<113> Artificial

<110>

<111> Artificial Sequence

<112> 1-43

<113> Synthetic construct.

<400> 178

gaagagaccag gatcatcaag gggttcgagt gcaagcctca etc 43

<110> 179

<111> 907

<112> DNA

<113> Homo sapiens

<400> 179

gagcagtggt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aaqaaaqagg agagcaacga agaagtgaat atagaagttt tgcattctcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200

atgacgcta cctggctaaa gacggctega aattctactg cagccggaca 250

caaaatnaag ggcaccccaa atggtttggt cttggtgttg ggcaagtcac 300

aaaaacata gacattccta tgacagatat gtgcctctga aaaaagcgaa 350

agtgattat gacatttca tttccattag gaaaggaagg ctatgaaaa 400

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<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

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Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	20	25	30	
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150	

155	160	165
170	175	180
185	190	195
200	205	210
215	220	

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

atattctctgct ggagccgatg cc 22

<410> 182

<411> 18

<412> DNA

<413> Artificial

<420>

<421> Artificial Sequence

<422> 1-18

<423> Synthetic construct.

<400> 182

agacatggaca atgacagg 18

<410> 183

<411> 18

<412> DNA

<413> Artificial

<420>

<421> Artificial Sequence

<422> 1-18

<423> Synthetic construct.

<400> 183

acttttcaggga tgaacagg 18

<410> 184

<411> 18

<412> DNA

<413> Artificial

4000> Artificial Sequence
4001> 1-18
4002> Synthetic construct.

4000> 184
atgtgtgtgcc accccaad 18

4010> 185
4011> 27
4012> DNA
4013> Artificial

4020
4021> Artificial Sequence
4022> 1-27
4023> Synthetic construct.

4030> 185
ggatccctgat atgacttgtc acgtggc 27

4040> 186
4041> 24
4042> DNA
4043> Artificial

4050
4051> Artificial Sequence
4052> 1-24
4053> Synthetic construct.

4060> 186
* aaagagaggg aagaggagtt gcac 24

4070> 187
4071> 52
4072> DNA
4073> Artificial

4080
4081> Artificial Sequence
4082> 1-52
4083> Synthetic construct.

4090> 187
accacattatg accgctacct gactaaagac ggctcgaaat tctactgcag 50
gc 12

4100> 188
4110> 573
4120> DNA
4130> Homo sapiens

4400> 188
cagaaatgta gaaacattg ctctcttcag gattctggtt ttgtgtgaga 50
ctcttgggaa ctgtgtctca gaaacaaa attctcttca ctaagtgcac 100

atgagatgct tctatcttct atgagatctc ctgagctatc gacatctctt 150
 atacttctgg atctggttctt aaactattca cacttccctt aaagctat ct 200
 atctccagggc atggtggtctc ggcgtctgaa tctcagttct ttgggaagcc 250
 aagtcaggtg gatcacctga cctcaggagt ttgagaccan ccttuccaac 300
 atautgaaac cccgtgtctc ctaaaaatac aaaaatcacc cgggcgtggt 350
 gttgcattgcc tgcattccca gttactcggg aggtcgagac aggagaatcg 400
 atttactca ggaggcagaa gttgcagtga acccagatcc tgcattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttggttc atttcagac tgcctctca gttgttctg ggateccctc 550
 ccataaaag tacttatatt etc 573

<210> 139
 <211> 74
 <212> PRT
 <213> Homo sapiens

<210> 139
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 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Lys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<240> 190
 agggaccatt ccttcttcca ggc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<400>
 <401> Artificial Sequence
 <402> 1-24
 <403> Synthetic construct.

<400> 191
 attacatgt ctccaaggag aata 24

<400> 192
 <401> 50
 <402> DNA
 <403> Artificial

<400>
 <401> Artificial Sequence
 <402> 1-50
 <403> Synthetic construct.

<400> 192
 cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcaatgc 50

<400> 193
 <401> 1091
 <402> DNA
 <403> Homo sapiens

<400> 193
 caagcaggtc atcccccttg tgaacttcaa agagaagcag agagaggaga 50
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 gactttggaa gtgacccacc atggggctca gcatttttt gtccctgtgt 150
 gttcttgggc tcagccagge agccacaccg aagattttca atggcaatga 200
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<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194
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 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
 125 130 135
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
 140 145 150
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
 155 160 165
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
 170 175 180
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
 185 190 195
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

20	210	220
Leu Gly Leu Val Ser Trp Gly Ser Val Gly Phe Tyr Gly Gln Asp		
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp		
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
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 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
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 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197
 <211> 4842
 <212> RNA
 <213> Homo sapiens

11 197

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 <213> Homo sapiens

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 35 40 45
 Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
 50 55 60
 Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
 65 70 75
 Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
 80 85 90
 His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
 95 100 105
 Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
 110 115 120
 Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
 125 130 135
 Thr Arg Leu Asp Leu Ser Gln Asn Gln Ile Gln Gly Ile Pro Arg
 140 145 150
 Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
 155 160 165

Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	170	175	180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg	185	190	195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu	200	205	210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp	215	220	225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr	230	235	240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp	245	250	255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro	260	265	270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr	275	280	285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu	290	295	300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu	305	310	315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr	320	325	330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	335	340	345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	350	355	360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	365	370	375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	380	385	390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	395	400	405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	410	415	420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	425	430	435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	440	445	450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser			

	455		460		465
Leu Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser			
	470		475		480
Lys Lys Phe Arg	Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe				
	485		490		495
Leu Ser Glu Cys	Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg			
	500		505		510
Cys Glu Gly Thr	Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg			
	515		520		525
Ile Pro Ser His	Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn			
	530		535		540
Asp Asn Glu Val	Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys			
	545		550		555
Leu Pro Asn Leu	Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys			
	560		565		570
Glu Val Arg Glu	Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu			
	575		580		585
Leu Met Leu Thr	Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val			
	590		595		600
Phe Arg Gly Leu	Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn			
	605		610		615
Leu Ile Ser Cys	Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser			
	620		625		630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr			
	635		640		645
Pro Gly Ala Phe	Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu			
	650		655		660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly			
	665		670		675
Lys Trp Leu Arg	Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys			
	680		685		690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala			
	695		700		705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln			
	710		715		720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val			
	725		730		735
Val Arg Cys Ser	Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met			
	740		745		750

Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr	
			771					760					765	
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile
			772					775					780	
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe
			785					790					795	
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg
			800					805					810	
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu
			815					820					825	
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu
			830					835					840	
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly
			845					850					855	
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu
			860					865					870	
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser
			875					880					885	
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr
			890					895					900	
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala
			905					910					915	
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr
			920					925					930	
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr
			935					940					945	
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile
			950					955					960	
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser
			965					970					975	
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly
			980					985					990	
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys
			995					1000					1005	
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys
			1010					1015					1020	
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile
			1025					1030					1035	
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys

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Tyr Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
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Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
Leu Leu Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Gln		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Gln		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Gln		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
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Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Gln Lys Asp Ser	1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp	1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly	1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu	1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn	1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser	1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly	1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg	1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala	1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln	1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln	1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu	1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser	1520		

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<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

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<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

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<22> Synthetic construct.

<400> 200
tttttggcat tggaggagag cag 24

<210> 201
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<222> 1-50
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<210> 302
<211> 153
<212> DNA
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<400> 302
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cgggcattct gacctcatt ggtgcctgg tcacaggcgc cgagtccaaa 200
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gta 793

<110> 145
 <111> 148
 <112> EST
 <113> Homo sapiens

<400> 203

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Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
				110					115					120
Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys	Lys	His	Cys	Glu	Gly
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Arg	Asp	Leu	Ser	Glu	Trp	Lys	Lys	Gly	Cys	Glu	Val	Ser		
				140					145					

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 <223> Synthetic construct.

<400> 104

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<110> 205
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 <222> 1-24
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<210> 107
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<210> 107
<211> Artificial Sequence
<212> 1-24
<213> Synthetic construct.

<400> 206
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<210> 107
<211> 24
<212> DNA
<213> Artificial

<210> 107
<211> Artificial Sequence
<212> 1-24
<213> Synthetic construct.

<400> 107
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<210> 108
<211> 47
<212> DNA
<213> Artificial

<210> 108
<211> Artificial Sequence
<212> 1-47
<213> Synthetic construct.

<400> 108
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<210> 109
<211> 1648
<212> DNA
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ttttttacc: tctgtctcgc atgtatccca gtgttcaggc tggctagacg 200
tgggagagac atctctctct atgttcaact cccatctctt ctctcagcca 250

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18 Arg Trp Val His Phe Ser Glu Ala Ile Gln Lys Phe Ile Arg
 275 280 285

290 Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
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310 Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
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Arg Tyr Val Thr Lys Leu Leu Val
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 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
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 35 40 45
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
 50 55 60
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
 65 70 75
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
 80 85 90
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
 95 100 105
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
 110 115 120
 His Met Arg Lys Lys Leu Tyr Gln Asn Gly Val Thr Asp Ser Leu
 125 130 135
 Lys Ser Asn Ile Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

141	141	151
Asp Lys Trp Leu Ser Tyr Pro Gln Thr	Gln His Val Pro Leu Ser	
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
185	190	195
Lys Asn His Gly Thr Val Trp Ser Gln	Ile Gly Lys Gly Phe Leu	
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Gln	
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val	
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu	
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln	
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg	
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro	
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp	
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly	
395	400	405
Thr Gln Glu Cys Pro Gln Leu Arg Phe	Ala Tyr Met Val Thr Thr	
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val	
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118 Arg Glu Glu Ala Thr Ile Thr Val Ser Lys Arg Tyr
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<210> 213
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<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
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 35 40 45

100	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr			
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110	Gly	Leu	Phe	Ala	Val	Gln	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val			
				65					70					75			
120	Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His		
				80						85				90			
130	Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp		
				95					100					105			
140	Gln	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu		
				110						115				120			
150	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu			
				125					130					135			
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<211> 216

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Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Ala Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130 135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140 145 150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
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Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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acttctcttg atgacacaga gggcagagac gggcctcttg tgaat'gaa 200

aatggatgaa atctaacctc actcagagaa catgggaat tcaatctaa 250
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<210> 218
 <211> 252
 <212> FRT
 <213> Homo sapiens

<400> 218
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 35 40 45
 Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
 50 55 60
 Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
 65 70 75
 Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
 80 85 90
 Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
 95 100 105
 Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
 110 115 120
 Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
 125 130 135
 His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
 140 145 150
 Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
 155 160 165
 Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
 170 175 180
 Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
 185 190 195
 Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
 200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Ile
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
 245 250

<210> 219
 <211> 2065
 <212> DNA
 <213> Homo sapiens

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 tatatgttaa aaaaa 2065

<210> 220
 <211> 231
 <212> PBT
 <213> Homo sapiens

<400> 230
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 20 25 30
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
 35 40 45
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
 50 55 60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				85					90					95	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<210>
 <211> Artificial Sequence
 <212> 1-20
 <213> Synthetic construct.

<400> 221
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<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<210>
 <211> Artificial Sequence
 <212> 1-24
 <213> Synthetic construct.

<400> 222
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<210> 223
 <211> 41

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
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<210> 224
<211> 992
<212> DNA
<213> Homo sapiens

<400> 224
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tatactcttc ctcatggcg gagctttctt ctggttggcg tctctactga 150
tttcgtacct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgcttg tctctgtcta 250
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ta 902

<210> 225
<211> 252
<212> FRT

0113 - Homo sapiens

04300 - 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	1	5	10	15
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	20	25	30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	35	40	45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	50	55	60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	65	70	75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	80	85	90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	95	100	105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	110	115	120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	125	130	135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	140	145	150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	155	160	165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	170	175	180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	185	190	195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	200	205	210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	215	220	225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	230	235	240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	245	250	255	

Ser Arg

02110 - 226

1111 3939
1112 DNA
1113 Homo sapiens

1400 226

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<210> 227
 <211> 832
 <212> FRT
 <213> Homo sapiens

<400> 227
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 1 5 10 15
 Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gin
 20 25 30

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11	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60
21	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
31	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
41	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
51	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
61	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
71	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
81	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
91	Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	170	175	180
101	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
111	Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	200	205	210
121	Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	215	220	225
131	Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	230	235	240
141	Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	245	250	255
151	Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	260	265	270
161	Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	275	280	285
171	Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	290	295	300
181	Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	305	310	315
191	Cys	Thr	Phe	Asn	Thr	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	320	325	330

332	342	352
Asp Arg Ala Cys Pro Gln Ser Gly His Pro Arg Val Leu Ala		
335	345	345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly		
350	355	360
Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser		
365	370	375
Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe		
380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val		
395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys		
410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala		
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe		
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val		
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn		
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly		
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile		
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile		
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu		
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr		
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys		
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met		
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro		
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile		
605	610	615

Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn
			625					625					630
Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr
			635					640					645
Leu	Leu	Leu	Ser	Thr	Glu	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys
			650						655				660
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr
			665						670				675
Gly	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met
			680						685				690
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala
			695						700				705
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu
			710						715				720
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile
			725						730				735
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu
			740						745				750
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe
			755						760				765
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu
			770						775				780
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp
			785						790				795
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly
			800						805				810
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val
			815						820				825
Arg	Asp	Lys	Ile	Tyr	Val	Phe							
			830										

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

gctcaagtgc cctgccttgc cccaccagc ccagcctggc cagagccccc 50

tggagaaga gctctcttct tgccttgcag ctggaccaag gaagccatc 100

cttgcctctt gagggcctct cctgacatg ctccctgcct gactgtact 150

ctctctctt tctctccccc agctctcttc caagggccac cctgagaga 200

ctatcttacc ctatctctt ctatcttacc ctatcttacc ctatcttacc 1700
 ctatcttacc ctatctctt ctatcttacc ctatcttacc ctatcttacc 1750
 ctatcttacc ctatctctt ctatcttacc ctatcttacc ctatcttacc 1800
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<210> 229
 <211> 807
 <212> FR1
 <213> Homo sapiens

<400> 229
 Met Val Pro Ala Thr Leu Thr Leu Leu Cys Val Ser Val Pro Gln
 1 10 15
 Ala Leu Trp Cys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20	25	30
Gln Asn Tyr Gly Gly Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro	35	40
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp	50	55
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser	65	70
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala	80	85
Gln Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val	95	100
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn	110	115
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu	125	130
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala	140	145
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe	155	160
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe	170	175
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly	185	190
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu	200	205
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala	215	220
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser	230	235
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro	245	250
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr	260	265
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu	275	280
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala	290	295
Gln Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Gln Asp	305	310

Pro	Ala	Ala	Pro	Leu	Gln	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				337					343					346	
Arg	Val	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	
				338					348					349	
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350					355					360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365					370					379	
Glu	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380					385					390	
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395					400					405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
				410					415					420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425					430					435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
				440					445					450	
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
				455					460					465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
				470					475					480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
				485					490					495	
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
				500					505					510	
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
				515					520					525	
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
				530					535					540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545					550					555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
				560					565					570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
				575					580					585	
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
				590					595					600	
Val	Asn	Asp	Ser	Gln	Gly	Trp	Leu	Cys	Ile	His	Lys	Phe	Ser	Gly	

615	620	625
Val Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp		
630	635	640
Leu Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu		
645	650	655
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His		
660	665	670
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
675	680	685
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
690	695	700
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
705	710	715
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
720	725	730
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
735	740	745
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
750	755	760
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
765	770	775
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
780	785	790
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
795	800	805
Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val		

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgcccttaccg cgcagcccca agattcacta tggtagaaat cgccttcaat 50

<210> 241

<211> 24

<212> DNA

<213> Artificial Sequence

<21>

<21> Artificial Sequence

<21> 1011

<22> Synthetic oligonucleotide probe

<400> 231

cctgactgtt aacccactc caga 24

<21> 232

<21> 23

<21> DNA

<21> Artificial Sequence

<22>

<22> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagttatct tct 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

ccggggacat gaggtggata ctgttcattg gggccttat tgggtccagc 50

atctgtggcc aagaaaaatt ttctgggac caadtttga ggattaatgt 100

cagaaatgga gacgagatca gcaaattga tcaactagtg aattcaaaca 150

acttgaagct caatttctgg aaatctccct cctcctcaa tgggcctgtg 200

gatgtcctgg tccatctgt cagtctgcag gcatttaaat ccttctgag 250

atcccagggc ttagagtagc cagtgcacat tgaggacctg caggcccttt 300

tagacaatga agatgatgaa atgcaacaca atgaaggga agaacggagc 350

agtaataact tcaactacgg gccttacct tccctggaag ctatttacca 400

cgagatggac aacattgccg cagacttcc tgacctggcg aggaggggtga 450

agattgaaca ttcttttgaa aaccggccga tgtatgtact gaagttcagc 500

acttggaag gctgaggcg gccggccgtt tggatgaatg caggcatcca 550

tcccgaaag tggatctcc aggcactac aatttggacg gcaaggaaga 600

ttgtatctga ttaccagagg gatccagata tcaactccat cttggagaaa 650

atggaatatt tctgttgcc tcttcccaat cctcatggat atgtgtatcc 700

tcaactcaa aaccgattat gaaggaaac ggggtccga aatcctgaa 750

ctctctatc tctctctgac ccaactaaa atttccacg tagttttgaa 800

ctcaatgag ctagggaaca ccttctctc gaattctac atggaacaa 850

agtgaatttg aatttgggt tgaatttgt ggtatattt atcctaaat 200
 atgggaattt caaagagttt atggaatttg aagatattt aagatgata 250
 atctatccat atgggtatct agtcaaaaag aacatagata cccaaagaaat 300
 aaacaagatg gagagggattg aggcctaaagc tctagattct gtgtcaggca 1050
 cttaagtaaca agtgggtacc aactgaacca ctgtctatcc agctaacggg 1100
 agaaacatcg actggggata taacaacggc atcaaatctt cattacacatt 1150
 tgaattgaga gataccggga cctatgactt cctcttgcca gctaaccaag 1200
 tcttccccac tgcagaggaag acgtggctgg ggctgaagac catcatggag 1250
 catctggggg acaacctcta ctaggcata cctctgctct gtctacattt 1300
 attttatccc acaactgacg gaactgaagc cattgtttaa gpagctcttt 1350
 cctacctgtg tgagtcagag cctcttggtt ttgtggagca cacaggcctg 1400
 cctctctcca gccagctccc tgagctgctg tgtcctggcg gtgtccctgc 1450
 aagaactcgt tctgccagcc tcttcaattt tggctctgct atttttgata 1500
 agccttttgt ctgtttctcc ttccacctg ctggctgggc ggtctcaact 1550
 agcatcacc cttctgggtg ggcattctct tctctacctt atttttagaa 1600
 ccaaagaaca tctgagatga ttctctaccc tcatccacat ctatccaaag 1650
 cagtgaacctt gctctgggtg cactgtggga gacaccactt gtctttaggt 1700
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 gaaaatatit tcttttgagc agcaaatctt gtagggatat cagtcaaggt 1800
 ctctccctcc cctctctctt gtttttttt tttttgagac agagttttgc 1850
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 ctctgctccc tgggttcaag caattctctt gctcagcct cttgaatagc 1950
 ttggtttata ggcgcattgc accatgcttg gctaatttt tgtttttagt 2000
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atctaaattg cagpatatgt gattatctt cactatctat atggatata 2350
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 aggtctaaa tcaactctct ggcctggata atctcactgc cctggcctat 2450
 tcccatttgt gctgtatgt atctgtgtt tcttgtctt gtttgcata 2500
 tgttgtgtg tgttgtgtg tgttgtgtt tgttgtgtg tatctatcta 2550
 tttgtatcc tggaccacaa attctaatg agagcaagaa ttcatctcc 2600
 agctgcctct tgtttcattt cactcagca cgtaccatct gttcttttgt 2650
 tgttgttgtt ttgttttgt ttttttgtt ttacaaaaca tatctgtaa 2700
 tcttaacctc ctgcctagga ttgtacagc atctggtgtg tctttataag 2750
 ccaataaata ttcaatgtg aaaaaaaaaa aaaaaa 2786

<210> 234
 <211> 421
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile
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 Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
 20 25 30
 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 35 40 45
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
 50 55 60
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
 65 70 75
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
 80 85 90
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
 95 100 105
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
 110 115 120
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
 125 130 135
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
 140 145 150
 His Ser Ile Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
 155 160 165

Asp Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile	170	185	190
His Ser Arg Gln Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala	185	190	195
Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser	200	205	210
Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro	215	220	225
Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys	230	235	240
Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro	245	250	255
Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp	260	265	270
Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu	275	280	285
Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn	290	295	300
Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met	305	310	315
Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu	320	325	330
Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val	335	340	345
Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr	350	355	360
Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile	365	370	375
Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly	380	385	390
Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr	395	400	405
Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu	410	415	420

Tyr

- *210- 235
- *211- 1743
- *212- HNA
- *213- Human sapiens

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Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe		
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met		
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn		
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe		
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala		
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys		
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser		
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala		
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser		
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser		
350	355	360
Alu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile		
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn		
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile		
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser		
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

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<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caacacatgca aggaagggtt agt 23

<217> 234

<211> 47
<212> DNA
<213> Artificial

<221>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgtgtt ggctctgtg ctccaacca tgcaaggaca gggagat 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<221>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgaatggggg tctcaaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<221>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
tggtatggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<221>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatctaac ctctatggag tactctttgc tgttggctc tgtgcacc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
cttgaaggt gctacattgc agggaggaa cctaaagaa cagagatcc 36

atgtgtccac ggcctgattc aatattcttt ccagggaacac aacgttggga 120
 gaacccagct cctggaagca ccagccttta tctcttcacac ttcaggtccc 150
 cttctcgaag aatcctctgt tctttgcctt cttaaagtcct ggtacatcta 200
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatccag 250
 aaaggaaaag ttctcttctt gtttggctta ctattgcatt tagaagctgc 300
 aacaaattcc aatgagacta gcacctctgc caacactgga tccagtgtga 350
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgaacctc 400
 agtgggggtc gcacagccac catctcaggg tccagcgtga cctccaatgg 450
 ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatac 500
 gcacagccac caactctgag ttcagccacg cgtccagtgg gatcagcata 550
 gccaccaact ctgagtcacg cacaaacctc agtggggcca gcacagccac 600
 caactctgag tccagccac cctccagtgg ggccagcaca gtcaccaact 650
 ctgggtccag tgtgaacctc agtggagcca gcactgccac caactctgag 700
 tccagccacg tgtccagttag ggccagcact gccaccaact ctgagtcag 750
 cacacctccc agtggggcca gcacagccac caactctgag tccagccaca 800
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 ggccagcact gccaccaact ctgagtcacg cacaaacctc agtggggcca 950
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 ctgagtcacg caggaacctc agtggggcca gcacagccac caactctgag 1150
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 cacaaacctc agtggggcca gcacagccac caactctgag tccagccacg 1250
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 agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350
 ggccaacaca gccaccaact ctgagtcacg cacagtgtcc agtggggcca 1400
 gcactgccac caactctgag tccagccaca cctccagtgg gatcagcaca 1450
 gccaccaact ctgagtcacg caaaacctcc agtggggcca acacagccac 1500

tttctctgag tccatgaaa cctccagtga ggcacacaa ggcacaaat 1440
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 tgaagaaggt attctcacc tttcttgcct ttaccagaca ctggaaagag 2200
 aatactatat tgcctattta gctaagaaat aaatacatct catctaacac 2250
 acacgacaaa gagaagctgt gcttgccccc ggtggygtat ctagctctga 2300
 gatgaactca gttataggag aaaacctcca tcttggactc catctggcat 2350
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
 <211> 526
 <212> PRT
 <213> Homo sapiens

<400> 243
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
 1 5 10 15
 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
 20 25 30
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
 35 40 45
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
 50 55 60
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
 65 70 75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				110					115					120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val
				125					130					135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				140					145					150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				155					160					165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				170					175					180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				185					190					195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				200					205					210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				215					220					225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				230					235					240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245					250					255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				260					265					270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				275					280					285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				290					295					300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				305					310					315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala
				320					325					330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				335					340					345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				350					355					360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala		
380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala		
395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala		
410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala		
425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val		
440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala		
455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala		
470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala		
485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile		
500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe		
515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn		
530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly		
545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro		
560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile		
575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro		
590	595	

<210> 244

<211> 26

<212> RNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

<110>: cctttatctc ttccgc 16

<110>: 145

<111>: 24

<112>: DNA

<113>: Artificial

<120>

<121>: Artificial Sequence

<122>: 1-24

<123>: Synthetic sequence.

<400>: 245

gtcagagttg gtggetgtgc tagc 24

<110>: 246

<111>: 48

<112>: DNA

<113>: Artificial

<120>

<121>: Artificial Sequence

<122>: 1-48

<123>: Synthetic construct.

<400>: 246

cgaccacaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<110>: 247

<111>: 957

<112>: DNA

<113>: Homo sapiens

<400>: 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcaccc 50

ttcccgacct tcccagcaat atgcaccttg cactcttggt cggctcctgc 100

tcctctcttc tgcctactgg ggccctgtct gcatgggggg ccagcgatga 150

ccccattgag aaggctattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcac 250

cccgggaagg aagtggagaa ggttttcaac ggaattagca acatggggag 300

ccacacccggc aaggagtttg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tggccatgag atcaaccatg gtattggaca agcaggaaag 400

gaannagaga agcttggcca tggggtcaac aacgtgctg gacaggccgg 450

gaannancca gacaaaggcg tccaagcgtt ccacactggg gtccaccagg 500

ctnnnancca accagagaaa ctgggcaaac gggtaacca tgcctgtgac 550

taattttaa aggaataga gaagattgac caagttccc accatgctgc 600

tttcttgggt gggatgggt tggatattt tttatagg gttttttaa gtt
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 tacacca 957

<210> 248
 <211> 247
 <212> FRT
 <213> Homo sapiens

<400> 248
 Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
 1 5 10 15
 Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
 20 25 30
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
 35 40 45
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
 50 55 60
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
 65 70 75
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
 80 85 90
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
 95 100 105
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
 110 115 120
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
 125 130 135
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
 140 145 150
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
 155 160 165
 Val Gln Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
 170 175 180

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
				215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
				230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
				245										

<210> 149

<211> 13

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<300> 149

caataatgat cttgcacgtc tgg 23

<400> 150

<410> 14

<412> DNA

<413> Artificial

<420>

<421> Artificial Sequence

<422> 1-14

<423> Synthetic construct.

<400> 150

aaagcttctt gcttcctttc ctgc 24

<410> 151

<411> 43

<412> DNA

<413> Artificial

<420>

<421> Artificial Sequence

<422> 1-43

<423> Synthetic construct.

<400> 251

agaccacatt gagaaggtca ttgaagggat caaccgaggg ctg 43

<210> 252

<211> 3761

<212> RNA

<213> Homo sapiens

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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Phe	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Gln	Ala	Gln	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Arg	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Gln	Ala	Leu

Pro	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Ile	Leu	Pro	Gly	Gly	Glu	Tyr
				105					110					105
Gln	Gln	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120
Pro	Leu	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile
				125					130					135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly
				140					145					150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn
				155					160					165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp
				170					175					180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala
				185					190					195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe
				200					205					210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro
				215					220					225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
				230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu
				260					265					270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile
				275					280					285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp
				290					295					300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp
				305					310					315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro
				320					325					330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr
				335					340					345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val
				350					355					360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys
				365					370					375

Asn	Val	Asn	Asn	Gln	Thr	His	Gln	Trp	Tyr	Thr	Val	Thr	His	Ile
343									348					351
Thr	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg
355									430					435
Gln	Asn	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Pro	Asp	Arg	Val	Leu
410									415					420
Asn	Ile	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	Val	Arg	Ser
425									430					435
Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	Val	Ala
440									445					450
Val	His	Arg	Val	Pro	Gly	Ileu	His	His	Thr	Tyr	Asp	Val	Leu	Phe
455									460					465
Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly
470									475					480
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly
485									490					495
Gln	Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu
500									505					510
Tyr	Ala	Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn
515									520					525
Cys	Ser	Leu	Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp
530									535					540
Pro	Tyr	Cys	Ala	Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu
545									550					555
Tyr	Gln	Pro	Gln	Leu	Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu
560									565					570
Gly	Ala	Ser	Ala	Lys	Asp	Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser
575									580					585
Pro	Ser	Phe	Val	Pro	Thr	Gly	Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln
590									595					600
Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	Leu	Ala	Cys	Pro	Leu	Leu	Ser
605									610					615
Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg	Asn	Gly	Ala	Pro	Val	Asn
620									625					630
Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr	Gly	Asp	Leu	Leu	Leu
635									640					645
Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	Trp	Ser	Leu	Glu
650									655					660
Val	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Gln	Val	Val

665	670	675
Leu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro	
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly Lys	
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val	
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe	
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln	
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys	Thr Cys Pro Val Val Leu	
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr	
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro	
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile	
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg	
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp	Ser Val Val	
830	835	

<10> 254

<11> 24

<12> DNA

<13> Artificial

<20>

<21> Artificial Sequence

<22> 1-24

<23> Synthetic construct.

<400> 254

agacatgca gaatctgctc ctgg 24

<10> 255

<11> 24

<12> DNA

<13> Artificial

<20>

<21> Artificial Sequence

<22> 1-24

<23> Synthetic construct.

<400> 255
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<400> 256
 <411> 18
 <412> RNA
 <413> Artificial

<420>
 <421> Artificial Sequence
 <422> 1-18
 <423> Synthetic construct.

<400> 256
 ctacaggctg cagttggc 18

<400> 257
 <411> 41
 <412> DNA
 <413> Artificial

<420>
 <421> Artificial Sequence
 <422> 1-41
 <423> Synthetic construct.

<400> 257
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<400> 258
 <411> 45
 <412> DNA
 <413> Artificial

<420>
 <421> Artificial Sequence
 <422> 1-45
 <423> Synthetic construct.

<400> 258
 gaaatgcaga tcttctcacc gggacagccc gtgcagaatc tctc 45

<400> 259
 <411> 4563
 <412> DNA
 <413> Homo sapiens

<420>
 <421> unsure
 <422> 3635
 <423> unknown base

<400> 259
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tggggggggc ggggtccccg gggggggggg gagggggggg gggggggggg 200
 aggggggggg gggggggggg gggggggggg atgggtcccc ctttaaggag 250
 tggggggggg gggggggggg gggggggggg aaaaaagggg gggggggggg 300
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 aattggggg gggggggggg gggggggggg gggggggggg gggggggggg 1400
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 ttcttttgtc tgggggtttc gacatgtttg tgagatttat gggaaaacttt 2150
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 ggagaaacta tgggtttggc atcagctga tttataaggg agatcttgtc 2600
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 atgtgtttt cttaataag actcctttca gatgagctt ttttttttt 3050

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 tttaaaaaaa tttttttttt ttagaacctt tgettaattt ctatggcaga 3200
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 agctttccag agttgataat ttctctctat ggtactctga taagcatggc 3450
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attatgtgtt agptgaaga attgtattat attttttat taagaacct 4810

aaacagaaa aa 4863

<210> 260

<211> #02

<212> FRT

<213> Homo sapiens

<400> 260

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Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys	Lys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	245	255
Gly	Arg	Lys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	260	270
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	275	285
Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala	290	300
Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu	305	315
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg	320	330
Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser	335	345
Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro	350	360
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu	365	375
Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly	380	390
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu	395	405
Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala	410	420
Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly	425	435
Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp	440	450
Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val	455	465
Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile	470	480
Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys	485	495
Arg	Ile	Asn	Gln	Glu	Ser	Gly	Ser	Leu	Ser	Phe	Leu	Ser	Asn	Ser	500	510
Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu	515	525
His	Lys	Gln	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu		

530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val	Glu
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met	Gln
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu	Glu
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe	Cys
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys	Arg
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile	Phe
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro	Ser
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg	Asn
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val	Arg
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu	Asp
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr	Phe
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val	Phe
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu	Gly
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu	Met
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn	Asn
785	790	795
Asn Gly Ser Val Arg Thr Ala		
800		

<210> 261

<211> 34

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtaccactac ggggtgtgga cgac 24

<210> 263
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 263
tgcatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccaggaagaag tcttcatga tgcacaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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tgacaccttc cctttgggac ttgaggttcc cagcctggtg gcccaggac 100
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tctttctagt tgcgcttttg ctatggcctt cgtctgtgac ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccagggtcgtg 300
agaaaaaato taactctcca aaacatgttt atttatatag atcaaaggga 350
tcaaatitta agpagctagt tacacatgga aaatttcaa ctgaaatga 400

50										51					60				
Phe	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Lys	Gly	Ser	Lys	Phe	Lys				
				81					81						75				
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu					
				86					85					90					
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly					
				95					100					105					
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro					
				110					115					120					
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala					
				125					130					135					
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu					
				140					145					150					
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val					
				155					160					165					
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro					
				170					175					180					
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu					
				185					190					195					
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Gln	Thr	Ala	Ile	Glu	Lys					
				200					205					210					
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp					
				215					220					225					
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala					
				230					235					240					
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu					
				245					250					255					
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala					
				260					265					270					
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro					
				275					280					285					
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile					
				290					295					300					
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp					
				305					310					315					
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val					
				320					325					330					
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala					
				335					340					345					

Leu Leu Lys Val Tyr
310

<210> 266
<211> 2403
<212> RNA
<213> Homo sapiens

<400> 266
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ttcatagtgt gagatccacc cacaggaata tccatggctt ttgtgctaat 150
tttgggtctc agttttctac agctgggtgc aaaaagtgcc caagtcactg 200
gaacggggcaa gtttgtccag gccttgggtg ggaaggacgc cgtgttctcc 250
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 <111> 466
 <112> PRT
 <113> Homo sapiens

<400> 267
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Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe		
50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser		
65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp		
80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr		
95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile		
110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly		
125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile		
140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala		
155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg		
170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile		
185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu		
200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu		
215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu		
230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile		
245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp		
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys		
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys		
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
305	310	315

Gln	Gln	Val	Irc	His	Ser	Gln	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	335	350
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

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<210> 168
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 168
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 agttcagta acagaagcat ggagtgttg tcatatgtc gttgatttgt 400
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 caggatcgtt ggtgggacag aagtagaaga gggtaaatgg cccctggcagg 650
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 gccacatggc ttgtgagtgc tgcctactgt tttaacaacat ataagaaccc 750
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 catgactatg atattttctt tgcagagctt tctagccctg tccctacac 900
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 tccagaaaga agcaagata tatcttatt ttcaattcga accaactact 1950

atgataaatg taaagaagat tctgtttttt tctgacctat aataattata 2080
 caaacttcac gcaatgtact tcttctaagg aaatttaaagg aatatattat 2090
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<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	230	235	240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	245	250	255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	260	265	270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	275	280	285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	290	295	300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	305	310	315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	320	325	330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	335	340	345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	350	355	360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	365	370	375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	380	385	390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	395	400	405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	410	415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
				20				25						30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35				40						45
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
				50				55						60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
				65				70						75

Leu	Ser	Ser	Pr	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

<219> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
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 tgccttggg agtaggatgt ggtgaaagga tggcgcttct ccttaacggg 200
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<210> 273

<211> 305

<212> FRT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
			20						25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
			35						40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
			50						55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
			65						70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
			80						85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
			95						100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
			110						115					120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
			125						130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
			140						145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
			155						160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

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	185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met			
	200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe			
	215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu			
	230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro			
	245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His			
	260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg			
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Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe			
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Gln Met Glu Glu Leu			
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<211> 1263

<212> DNA

<213> Homo sapiens

<400> 174

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<212> PRT

<213> Homo sapiens

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Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
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Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
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His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
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Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
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Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
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Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
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Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Tyr Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

265

Gly Ser Asp Lys	Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys	260	265	270
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Ile Ala Leu Met	Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val	335	340	345
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Val Thr Glu Lys	Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His	Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr	410	415	420
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Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	195
				185					190						
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	210
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Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	225
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Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	270
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220

230

310

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305 310 315

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320 325 330

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335 340 345

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350 355 360

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380 385 390

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Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val
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Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr
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Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly
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Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala
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270

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Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
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4212> DNA
4213> Artificial

4120>
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4122> 1-45
4123> Synthetic construct.

4400> 280
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4110> 281
4111> 320
4112> DNA
4113> Homo sapiens

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				115					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Ile	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

263	265	272
Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn		
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu		
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu		
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys		
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn		
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His		
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile		
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu		
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys		
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu		
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser		
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser		
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr		
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp		
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu		
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala		
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr		
515	520	

<210> 283
 <211> 24
 <212> RNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 283
 t g t t t t g g t c a c c t a c c c a a g g 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 t t a g g t g g t c t c c a a a g a g a g g g 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
 c t t a a g a t g t c c a c c t g g c t g c a a a t g t g a a a t t g t g g a c t g g 45

<210> 286
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 286
 g g g t g t t t g a t t t g t g g g g a t t t t t g a a g a g a g g a a t a g g a c c a a g g 50
 g t t t g a g g g g c t g c c t c t g g c a t a t g c a c a c a c t c a c a c a t t c t g t c a c a 100
 c c c g t c a c a c a c a c a t a c c a t g t t t c t c c a t c c c c c a g g t c c a g c c c t c a 150
 g t g t g t c c c a t c c a g c a g g g e t a c c c t g a a g t c t g g c t g c a g c c c t c c 200
 c g t c a g t g g g c a g g c g g g c t t c a t c c c t c c t t t c t c t c c c a a g c c c a a c 250
 t g c t g t c a c t g c a t g t c t g c c a a g g a g g a g g g a a c t g c a g t g a c a g c a g 300
 a a g t a a g a g t g g a g g a g g a c a g a g c t g g g a c a c a g g t a t g g a g a g g g 350
 a t t c a g a g a g c a t a g a g a g a g c a g a g a t a t c a g g t g c c g a c a g t g a a t 400
 c a g g a g a g a g a g g a 450

aggttccaaa accctccagc catgttccga tccctccaa actgctccac 550
 aggtccccca caccgtcccg agctgcctt gcttctagtg attctggccc 600
 tgggggcccg gtgggcccag gaggggtcag agcttgctct gctggagggg 650
 gactgcctgg tggtctgtga gctggccga gctgctgcag gggggcccgg 690
 gggagccagc ctgggagagg caccctctgg ccgagtgcca tttgctggg 700
 tccgaagcca ccaccatgag ccagccgggg aaaccggcaa tggcaccagt 750
 ggggcccctc acttcgacca ggtcctgggt aacgagggcg gtggcttga 800
 ccgggctctt ggtcctcttg tagccctgt ccgggggtgt tacagcttcc 850
 ggttccatgt ggtgaagggt tacaaccgac aaactgtcca ggtgagcctg 900
 atgtgaaca cctggcctgt catctccagc ttgccaatg atctgacgt 950
 gacccgggag gcagccacca cctctgtgct actgccttg gacccgggg 1000
 accgagtgtc tctggcctg cgtgggggga atctactggg tggttggaaa 1050
 taactaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100
 ttccaagcac aa-gaatccag cccctgacaa cttctctctg cctctcttg 1150
 ccccagaaa agcagaggga ggagagagac tccctctggc tcttatccca 1200
 cctcttctga tgggaccctg tgcacaacac ccaagttaa gagaagagta 1250
 gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300
 cctccccagc cactgctgc atctgttctt gctgcagcc ctaggatcag 1350
 ggcaaggttt ggcaagaagg aagatctgca ctactttggg gctctgctc 1400
 ctccggttc cccaccccag ctctctgctc aatgctgate agggacaggt 1450
 ggccaggtt agctgacag gcccacacag gagcccagat ggacaagcct 1500
 cagcgtacc tgcaggcttc ttctgtgag gaaagccagc atccaggatc 1550
 tcagccagca cctccagaag ctgagccagc accgtatggg ctagggtggg 1600
 aggtccagcc acaggcagaa ggggtgggaag ggcctggagt ctgtggctgg 1650
 tgaggaaagga aggaggggtg attgtctaga ctgaacatgg tacacattct 1700
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtcctctat 1750
 gctggatccc agatggactc tggcccttac ctcccacct gagattaggg 1800
 tgagtgtgtt tgctctgctt gggagcagag ctgagagcag atacagag 1850
 ctggaaatgg acatggaaa acatcgataa ccattccatc tctgtctgg 1900

caacctctctg aaactgctcc acctttgaag tttdaaccttt agtccctcca 1950
 cactctgaat gctgctctct tctcccagc tctctcaactg agtctatcttc 2000
 actgtactctg ttccagcata tcccactat ctctctttct cctgatctgt 2050
 gctgtcttat tctctctctt aggtctctta ttacctggga ttccatgatt 2100
 cattcttca gacctctcc tgcagtatg ctaaacctc cctctctctt 2150
 tcttatcccg ctgtccatt ggcacagct ggtgtaat atcaataaaa 2200
 caactagaga atggtggta gtgagacact atagaattac taaggagaag 2250
 atgctctgg agtttgatc ggggtgtaca ggtacagta ggtatgttc 2300
 agaggaaaat aaatatcaa ctgtatacta aaattiaaaa 2340

<210> 287
 <211> 295
 <212> PRT
 <213> Homo sapiens

<400> 287
 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser
 1 5 10 15
 Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly
 20 25 30
 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
 35 40 45
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
 50 55 60
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
 65 70 75
 Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn
 80 85 90
 Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu
 95 100 105
 Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val
 110 115 120
 Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn
 125 130 135
 Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val
 140 145 150
 Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala
 155 160 165
 Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

	170		175		180
Leu	Arg	Leu	Arg	Arg	Gly
				Asn	Leu
				Leu	Gly
				Gly	Trp
				Lys	Tyr
				Ser	
				185	190
Ser	Phe	Ser	Gly	Phe	Leu
				Ile	Phe
				Pro	Leu
				200	205

<212> 236
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 -gggagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 -ctagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 -ctgtgtact gccctggac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tgcggccacc actggccgcc ggcgcagct ccaggtgtcc 50
 tagagggcca gctcggacc cgtcccgagg cccctgtgt ctgcgcgaag 100
 cctgtgcg ccgggggggg gcatgggcca gggggggg gtgaagcgcc 150

tcccccggg ggcgtgaattc ggggggcttc aacatgaag accctcatag 200
 ccaattactc gggggtcttg cggggggagc gtcaggccga ggttgaacgg 250
 agccagcgcct ctccaggagc accctccgtg tggcggagcg ggtctgggag 300
 atggggcaat agatccagca tctctccgc cctccaggac ctctctcttg 350
 tcacctagct caataggctc aaggtggaaa agagctaca ggtcatctca 400
 gtgctccagt ggcctctgtc ctctcttcta ctgggagtg cctgcaatgc 450
 cactctcatg tacatatctt gcactgattg ctggctcctc gctgtgctct 500
 acttcaattg gctgggtgtt gactggaaac cacccaagaa aggtggcagg 550
 aggtcacagt gggctcgaaa ctgggctgtg tggcgtact ttcgagacta 600
 ctctccctc cagctgggtg agacacacaa cctgctgacc accaggacct 650
 atatctttgg ataccacccc catgggtatca tgggcttggg tgcctctctc 700
 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcataac 750
 gcttcaactg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800
 agtacctgat gtctggaggt atctgccttg tcagccggga caccatagac 850
 tatttgcttt caaagaatgg gactggcaat gctatctca cctggttggg 900
 gggtgccgct gactctctga gctccatgcc tggcaagaat gcagtcaccc 950
 tgggaaaccg caagggcttt gtgaaactgg ccttggtcca tggagctgac 1000
 ctggttccca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050
 ctctgaggag ggtctctggg gcgatgggt ccagaagaag ttccagaaat 1100
 acattgcttt cggcccatgc atcttccatg gtogaggcct ctctctctcc 1150
 gacactggg ggtcgtgtgc ctactccaag cccatcacca ctgttctggg 1200
 agagccctc accatccca agctggagca cccaaccag caagacatcg 1250
 aactgtacca caccatgtac atggaggccc tgggtgaagct ctctgacaag 1300
 cacaagacca agttcggcct cccggagact gaggctctgg aggtgaactg 1350
 agccaqctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400
 tttctctgt aaatttggaa gtgtcatggg tctctgtggg ttatttataa 1450
 gaaattataa caattttgct aaacccaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaaa aaaaaaaaaa 1570

210> 292
 211> 293
 212> 1RT
 213> Homo sapiens

400> 292
 Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu
 1 5 10 15
 Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
 20 25 30
 Ala Leu Ser Arg Gln Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180
 Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
 185 190 195
 Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
 200 205 210
 Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
 215 220 225
 Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
 230 235 240
 Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
 245 250 255
 Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 atgacgtgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 295
 aagatgaat tgtacaaagc aggtgatatt cgaggagggc tcttgggggc 50

<210> 296
 <211> 3060
 <212> tRNA
 <213> Homo sapiens

<400> 296
 ggggtcggg atggggggcg gggggggcg ggcgcgcact cgtcgaggcc 50
 cggacacagg gcggggcggg gccacggggc gaggagcgcg ggggcacag 100
 cggggcgcgcg gaggcgacgc cggggacgdc cgcgcgacga gcaggtggcg 150
 cgggcgcgag gcttgtccag ccggaagccc tgagggcagc tgttccact 200
 cggctctgctg accttctgdc ttggaaggct gtctccagcg aggggcgctg 250
 caccgctccc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300
 gtcctgctg caccctgctgg tcggctttgt ctctgtggcg agtcgtctgg 350
 tcatccactt cgtccagctg tgcacgctgg cgtctctggc ggtcagcag 400
 cagctctacc gcgcctcaa ctgcgcctc gcctactcac tctggagcca 450
 actcgtcatg ctgctggagt ggtggtctct caccgagctg acactgttca 500
 cggacacaggc caccgttagg cgttttggga aggagcagc agtcacccac 550
 ctcaacacaa acctcgagat cgaacttctc tctgggtgga ccctgtgtga 600
 gcgcttcggga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650
 tctcgtgccc cctcctcggc tggacgtggt accttctgga gattgtgttc 700
 tgcacacggga agtgggagga ggacggggac accgtggctg aagggtgag 750
 ggcgcctgctg gactaccccg agtacatgtg gtttctctcg tactgcgag 800
 ggacggtctt caccgagacc aagcaccccg ttagcatgga ggtggcggt 850
 gctaacgggc ttcctgtctt caagtaccac ctgctgcgcg ggaccaaggg 900
 ctccacacac gcagtcagt gcctccggcg gacagtcgca gctgtctatg 950
 atqtaacctt gaacttcaga ggaaacaaga acccgctcct gctggggatc 1000
 ctctacggga agaagtacga ggcgacatg tgcgtgagga gatttctct 1050
 ggaagacatc ccgtggatg aaaaggaagc agctcagtggt ctccataaac 1100
 tgtaccadga gaaggacgcg ctccaggaga tatataatca gaaggcctat 1150

ttctcagggg aaaaatttaa gactgacggg aacacgttga cactcctgaa 1200
 attcctgtcc tgggcacaca ttctcctgtc tcccctcttc agttttgtct 1250
 tgggcgtctt taaagaggga tcaactctcc tgcctcctgac ttctctgggg 1300
 ttgtgaggag cagcttcctt tggagttcgc agaactgatag gagaatcgct 1350
 tgaacctggg aggtggagat tgcagtgagc tgagatggca tcaactgtact 1400
 ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaacaa 1450
 aaaaaaccca gaattctgg agttgaactg tgtagttact gacatgaaaa 1500
 attcactaga ggcctgaacag cagatttgag caggcagaaa aaaatcagca 1550
 agcttgaaga tggtaacctg agatttttca ggctaataaa aaaagaatga 1600
 aggaataatta acagcctcag agaccctagg tgcacccgtca cacaatacaa 1650
 catatgcctg atgagagctc cagaaggaga ggagagaaaag ggtcagaaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctacccactc aggaagctca 1750
 gtgtaactca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaatg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaggat ctttgatcag attaacagct catttctcct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aacctcaac tgaattatt ggaactttga gtcttagatg gtcttgacct 2000
 ctttgtcttc agggacagtt tttaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggcagg gcacagtggc 2100
 ttacacctgt aatccagca ctttgggagg cccagacggg tggatcattt 2150
 ggggtcaggg tcatctcaaa ctctcagtt caggtgatct gcccgctca 2200
 gctcccaaa gtgttgtgat tgcaggcgtg agccactgag cctggccgga 2250
 atttcttttt aaggctgaat gatgggggcc aggcacgatg gctcagcct 2300
 gtgatcccaa gtacgttga ttgtaaacat gcaccacct gctggctaa 2350
 ttttgttatt tttagtagag acgtgttagc caggtgggtc tcatctcct 2400
 gacctcaagt gaccactgc ctacgcctcc caaagtactg ggattacagg 2450
 cgtgagccac tggcctggc cttgagcacc ttctgatgtg cttattggcc 2500
 atttgatat ctctatctt ctttggggaa atctctgttc aagtccttg 2550
 cttttttaa cttttttat ttattattt atttattttg agacagttc 2600

tttttttt tttttttt tttttttt tttttttt tttttttt 2650
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 tttttttt tttttttt tttttttt tttttttt tttttttt 3000
 tttttttt tttttttt tttttttt tttttttt tttttttt 3050
 tttttttt 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1 5 10 15
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
 80 85 90
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
 95 100 105
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
 110 115 120
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
 125 130 135
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
 140 145 150
 Asp Asn Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
 155 160 165

Trp	Ala	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Pyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttctctcgt aggtggacca tctg 24

<210> 296

<211> 21

<212> DNA

<210> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gggaactcca tgcataagga g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgcataaga gagctgcctt acgtgccctt cctcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatatcttt atttitaaga atctgaagta ctatgcata ctccctccaa 50

tgtcctgggg cagccaccag gcatactcat ctttgttgtt gtttttcttt 100

tgttttagca ctggggcaat tcttgcttat ttcttttgta ggaaaggggc 150

tcagtttgta ttgtgggggt ggtggcagga aggcgggctt acgcctgata 200

cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctggggg ctgaacactg ctccctcagt aaaattcctg ggatctgcct 300

atacctcttt ttctctaacc tggcataacc tgcttaaaga ctctcagggc 350

ttctctctgt tcttaggata aaactattta gagctacaag agccctcatg 400

atctggcccc tgcctccctg gccagcttca ttgtacatgt ggtgttctct 450

tgtctttcat gtaatgtggt atgcatggg gtctttgcac aagcctttcc 500

tctttgctg gacactgttc cctgcccccc ccatactctt cctacttaat 550

atgtatcat cctgcagatt tcaattctaa catcattttc tccagggata 600

ctgggtgac agaattctat cttgttttaf gctctcataa gaccacttgt 650

ttctttttt cagcattgtt cacttaattt tatctttcatg tgcgtttatg 700

ttctatgaa tctttctgt tcttcagatt gccagctctt gaactgcctg 750

aggttcaaa gatttctat tcttccaaa tatagtgcct acattatg 800
 tttgtctat ttttagaac tcaatggagg aggagatga gaaagattg 850
 aattctata gtttcaaaa tttgttagg ccacagattg taatttcaa 900
 atttactgt gatttgtgat tatctggga tgcaggtcct gattcagtag 950
 gccagattg ggcattctta acaaaatccc acgtgatgc catctctgac 1000
 ctatgaacta taataaatat taagaatcta tggagccagg ctgggcatgg 1050
 ttgttcaaa ctatgatccc aacattttgg gaggtgagg caggtctatc 1100
 aactogagtc aggaattcaa gactagcctg gccaacatgg tgcaccccca 1150
 tctgtactaa aaatacacia attagctggg catggttgga catcctgta 1200
 atcccagcta cttggggagg tgaagcaaga gaatcgcttg aacctgggag 1250
 ccggaggttg cagtgaagcc agatcaagcc actgtattcc aaccagggtg 1300
 acagaatgag actctatgac caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5				10						15

His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
			20					25						30

Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
			35					40						45

Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
			50					55						60

Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
			65					70						75

Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
			80					85						90

Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
			95					100						105

Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
			110					115						120

Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
			125					130						135

Tyr	Gly	Val	Leu	Leu	Ser	Ile	Leu
-----	-----	-----	-----	-----	-----	-----	-----

+210+ 303
 +211+ 1768
 +212+ DNA
 +213+ Homo sapiens

+400+ 303
 gactggaacta gaactcccttg tcccaagtda tccacccgcc tccagcctccc 50
 aagggtgctgt gattataatt gtaagccacc gtgtctcggcc tctgaacaaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatcctgtgg tggctagtgc tctactcct acctacatta aatctgttt 200
 ttctttctct tgaactaga ctttaacctt ctaaacacaga ggtctgtca 250
 ctctggctct ggcacaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctacccac accgtccctt cgaagccggg gacagcctca cttgctggc 350
 ctctcctgg agcagtgcac tcccaactg tctcagctct ggaggcactg 400
 actcgggcag tccaggtaga tgagcctctt ggtagctggc gctttcaagg 450
 tgggccttgc cctggccgtc gaagggatig acaagcccca agatttcata 500
 agcgatagct cccactgcac agcctnaga cttgctgtag tcaatcactg 550
 cctcggggcc aggaagggcc gtggacacct gctcagaagc agtgggtgag 600
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 gctgtggctc agaccagaa gggctctgct taccacacct ggtttatgtg 750
 acaggacttg cattctcctg gaacatgagg gaacgcggga ggaaagcaaa 800
 gtggcaggga aggaacttgt gcaaaattat gggtcagaaa agatggaggt 850
 gttgggttat cacaaggcat cgagctcctt gcattcagtg gacatgtggg 900
 gaaagggttg ccgatgggc atgacacact cgggaactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccagc taccagctgc tgaagggcaa 1000
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 ctacccctct tccctctgag aggcctcctt atgtccctac taaagccacc 1150
 aaaaacat aatgataat gttatgac tcaatgttag ccaggaagt 1200
 aaaaacat aatgataat gttatgac tcaatgttag ccaggaagt 1250

tgcctccagc aattacggtt tccatctc ccagcacaat cactgtgtat 1310
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 agctagaggt tgcctcaaat gatctccaaq ggcctttata ccccaggaga 1400
 ctcttgatttg aatttgaaac cccaaatcca aacctaaqaa ccagggtgcct 1450
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 gaggccgagg cccctagatc acctcaggtc agcgattcaa caccagcctg 1550
 gccaacatgg tccaacccct gtctctacta acaatacaaa aaaactadcc 1600
 aggcattggt gtctgtgctt gtatcccagc tactcgggag cctgagacag 1650
 gagaattact tgaacctggg aggtgaagga gctgagaca ggagaatcac 1700
 ttcagcctga gccacacagc gagactctgt ctccagaaaa ataaaaaaad 1750
 aattatgggt atttgtaa 1768

<210> 394
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 394
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
 1 5 10 15
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 282
 <212> FNA
 <213> Homo sapiens

<400> 305

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 tgcactgac tccagaggac tcttccagc gcatgacac agccattgac 100
 cccattctac ctacagagc cagtggacat ggcctcagc gcaatggagc 150
 ccgactttag cactggctc ttctaggga ggcgttccc cccatggaga 200
 ggcagagag agcagtgcct gcttccccc gaggaagac gactgtgca 250
 gtatcttttg agccgtcca tgcaggaga cccagcgtg cgaagctca 300
 ggtgtgtac cctggagcag ccgaggggg attctatgat gactggag 350
 caggcccaga tcttggcaa cctggcggg ctctccaga ccaagaagac 400
 gctggactg agcacttca cgggtactc cccctgac ctgacctgg 450
 cgtgcccgc ggaaggggc gtggtgacct ggaagtgga cgcacagccc 500
 ccggagctgg gacggccct gtggaggcag gcagaggcg agcacaagat 550
 cgaactccgg ctgaagccc ccttggagac cctggaagag ctgctggcg 600
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 aactgtccg cctactaga ggcgtgctg cagctgctg gacccggagg 700
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 cggcgggag tcagggtcta cctcagctc ctgcccctgg gcatggact 850
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 cttaagtgg gctgggacac aaaaaaaaa aaaaaaaaa 989

<10> 306
 <11> 262
 <12> PRT
 <13> Homo sapiens

<400> 306
 Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala
 1 5 10 15
 Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe
 20 25 30
 Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys
 35 40 45
 Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
 50 55 60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu	65	70	75
Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln	80	85	90
Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys	95	100	105
Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu	110	115	120
Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val	125	130	135
Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala	140	145	150
Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu	155	160	165
Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp	170	175	180
Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr	185	190	195
Glu Arg Cys Leu Glu Leu Leu Arg Pro Gly Gly Ile Leu Ala Val	200	205	210
Leu Arg Val Leu Trp Arg Gly Lys Val Leu Glu Pro Pro Lys Gly	215	220	225
Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg	230	235	240
Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly	245	250	255
Leu Thr Leu Ala Phe Lys Ile	260		

<310> 307
 <311> 2272
 <312> DNA
 <313> Homo sapiens

<400> 307
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 ctctcgccgt cagcatgccca cagccttcca agcccgggga cttgggtgttc 100
 gctaagatga agggctaccc tcactggcct gccaggatcg accacatcgc 150
 ggatggcgcc gtgaagcccc caccacaaca gtacccatc tttttctttg 200
 gacacacga aacagccttc ctgggaacca aggacctgtt cccctaagaa 250

aaatgtaaaag acaagtacgg gaagccccac aadagaaaag gcttcaatca 300
 agggctgtga gagatccaga acaaccccca cgcagctac agggccctc 350
 cgcagtgag ctctccagac agcgaggccc ccgaggccaa ccccgccac 400
 ggcagtgaag ctgacgagga cgatgaggac cgggggggtca tggccctcac 450
 agcgttaacc gccacagctg ccagcgacag gatggagagc gaactcagaat 500
 cagacaagag tagcgacaac agtggcctga agaggaagac gcttgcctca 550
 aagatgtcgg tctcgaaaac agcccgaaaag gcttccagcg acctggatca 600
 ggcacagctg tcccctcccg aagaggagaa ctcggaagc tcatctgagt 650
 cggagaaagc cagcgacacg gaattcacac ctgagaagaa agcagcggtc 700
 cgggcgcacc ggaggggccc tctgggggga cggaaaaaaa agaaggcgcc 750
 gtcagcctcc gaactcgaat ccaaggccga ttcggaacggg gccaaagcctg 800
 agccgggtggc catggcgagg tgggggtcct cctctctctc ttctctctcc 850
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 ccggcggcgg ccgagagcag aggaggagct gggcgccctg cgggagcagg 1100
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 gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgta 1400
 aggtggagcg gacccggaag cggtcagag gcttctcgat ggacaggaag 1450
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 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcccgctta 1650
 taaagcgacc aaggacgtac tggagaagcc accagaagtc tatacccgcc 1700

taaagtcagg tctctctgag ccaaaatctt aggggtttt aaatttgat 1750
 aaggttgaa tagagaaa aaaggctttt agaaattgt cgtttatga 1800
 gctggccggg aaggaggccc cccaggaaa ggcggagac aagccatga 1850
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 aaggtgtggc tctctgaaq acctgcacga cagcgtacgg gaggttccc 2000
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 gcccocggcc gagctcagge tgcctctctc ctcccccggc tgcagggaga 2150
 gcagagcaga gaactgtggg gaacgtgtg ctgtttgtat ttgttccctt 2200
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 actataaaacg gttttttaat ga 2272

<210> 308
 <211> 671
 <212> PRT
 <213> Homo sapiens

<400> 308
 Met Pro His Ala Phe Lys Pro Gly Asp Leu Val Phe Ala Lys Met
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 Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp
 20 25 30
 Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
 35 40 45
 Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
 50 55 60
 Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
 65 70 75
 Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
 80 85 90
 Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
 95 100 105
 Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
 110 115 120
 Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
 125 130 135
 Ala Ser Asp Arg Met Ala Ser Asp Ser Asp Ser Asp Lys Ser Ser

140	141	142
Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser		
155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala		
170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu		
185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala		
200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys		
215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser		
230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser		
245	250	255
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val		
260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro		
275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser		
290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu		
305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg		
320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln		
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Arg Glu Arg Ala Asp Arg Gly		
350	355	360
Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly Asp Glu Leu Arg		
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly		
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu		
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser		
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg		
425	430	435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr	440	445	450
Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys	455	460	465
Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser	470	475	480
Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg	485	490	495
Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser	500	505	510
Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys	515	520	525
Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala	530	535	540
Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile	545	550	555
Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys	560	565	570
Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala	575	580	585
Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala	590	595	600
Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu	605	610	615
Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg	620	625	630
Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro	635	640	645
Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala	650	655	660
Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser	665	670	

<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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cagactcaat gattatattc aattaacacc atttgacaga aaacattggt 100

tttatcatga atctatataa gnatcaaaac tttaaaagca aaatcaaaa 150
 ttttaacott tttcctgott tgatgatget aagcatgacc atgttggttt 200
 ttccagtcac tggcaactttg aagcaaaaata ttccaagaact caagctaaac 250
 tacaaaagaat tgcctgtttc aaatagctgt atctcctttt tgggttcact 300
 agaaggactg gattttcaaa ctctctctctt agatgaggaa agaggcagge 350
 tgcctctggg agcaaaagac cacatctttc tactcagctt ggttgactta 400
 aacaaaaatt ttaagaagat ttattggcct gctgcaaaag aaagggtgga 450
 attatgtaaa ttagctggga aagatgcaa tacagaaatgt gcaaatctca 500
 tcagagtact tcagcctat aacaaaactc acatataatgt gtgtggaaat 550
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 ggatattata ttcaaaactag acacacataa tttggagtct ggcagaactga 650
 aatgtccttt ccatcctcag cagccttttg cttcagtaat gacagatgag 700
 tactctact ctggaacagc ttctgatttc cttggcaaaag atactgcatt 750
 cactcgatcc cttgggccta ctcatgacca ccactacatc agaactgaca 800
 tttcagagca ctactggctc aatggagcaa aattttactg aactttcttc 850
 ataccagaca cttacaatcc agatgatgat aaaatatatt tctctctctg 900
 tgaatcatct caagaaggca gtactcaga taaaaccatc cttctctgag 950
 ttggaagagt ttgtaagaat gatgtaggag gacaacgcag cctgataaac 1000
 aagtggagca cttttcttaa ggcacagactg atttgctcaa ttcttggaag 1050
 tgatggggca gatacttact ttgatgagct tcaagatatt tatctactcc 1100
 ccacaaagaa tgaagaaaat cctgtagtat atggagtctt tactacaaac 1150
 agctccatct tcaaaggctc tgcctgttgt gtgtatagca tggctgacat 1200
 cagagcagtt tttaatggc catatgctca taaggaaagt gcagaccatc 1250
 gttgggtgca gtatgatggg agaattcctt atccacggcc tggtaaatgt 1300
 ccaagcaaaa cctatgacc actgattaag tccaccagag attttcaga 1350
 tgatgtcact aatttcataa agcggcactc ttgatgtat aagtccttat 1400
 acccagttgc agnaggacca acgttcaaga caatcaatgt ggattacaga 1450
 ctgacacaga tagtgttga tcatgtcatt aaagaagata ccagtaaga 1500
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 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Gln Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

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Phe Leu Leu Ser Leu Val Asp Leu Asn Lys Asn Phe Lys Lys Ile	100	105
Tyr Trp Pro Ala Ala Lys Glu Arg Val Glu Leu Cys Lys Leu Ala	110	115
Gly Lys Asp Ala Asn Thr Glu Cys Ala Asn Phe Ile Arg Val Leu	125	130
Gln Pro Tyr Asn Lys Thr His Ile Tyr Val Cys Gly Thr Gly Ala	140	145
Phe His Pro Ile Cys Gly Tyr Ile Asp Leu Gly Val Tyr Lys Glu	155	160
Asp Ile Ile Phe Lys Leu Asp Thr His Asn Leu Glu Ser Gly Arg	170	175
Leu Lys Cys Pro Phe Asp Pro Gln Gln Pro Phe Ala Ser Val Met	185	190
Thr Asp Glu Tyr Leu Tyr Ser Gly Thr Ala Ser Asp Phe Leu Gly	200	205
Lys Asp Thr Ala Phe Thr Arg Ser Leu Gly Pro Thr His Asp His	215	220
His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly	230	235
Ala Lys Phe Ile Gly Thr Phe Phe Ile Pro Asp Thr Tyr Asn Pro	245	250
Asp Asp Asp Lys Ile Tyr Phe Phe Phe Arg Glu Ser Ser Gln Glu	260	265
Gly Ser Thr Ser Asp Lys Thr Ile Leu Ser Arg Val Gly Arg Val	275	280
Cys Lys Asn Asp Val Gly Gly Gln Arg Ser Leu Ile Asn Lys Trp	290	295
Thr Thr Phe Leu Lys Ala Arg Leu Ile Cys Ser Ile Pro Gly Ser	305	310
Asp Gly Ala Asp Thr Tyr Phe Asp Glu Leu Gln Asp Ile Tyr Leu	320	325
Leu Pro Thr Arg Asp Glu Arg Asn Pro Val Val Tyr Gly Val Phe	335	340
Thr Thr Thr Ser Ser Ile Phe Lys Gly Ser Ala Val Cys Val Tyr	350	355
Ser Met Ala Asp Ile Arg Ala Val Phe Asn Gly Pro Tyr Ala His	365	370

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Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
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Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
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Ile Val Lys Leu Thr	Leu Asn Val Ile	Glu Asn Glu Gln Met	Glu		
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Asn Thr Gln Arg Ala	Glu His Glu Glu	Gly Gln Val Lys Asp	Leu		
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Leu Ala Glu Ser Arg	Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile	Leu		
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Ser Ser Pro Asn Phe	Ser Leu Asp Gln	Tyr Cys Glu Gln Met	Trp		
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His Arg Glu Lys Arg	Arg Gln Arg Asn	Lys Gly Gly Pro Lys	Trp		
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<220>

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<222> 1-25

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<400> 311

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<210> 312

<211> 24

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<222> 1-24

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<220>

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<222> 1-45

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<210> 314

<211> 3934

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<213> Homo sapiens

<400> 314

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<211> 370

<212> FRT

<213> Homo sapiens

<400> 315

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<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 317
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 20 25 30
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 35 40 45
 Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
 50 55 60
 Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
 65 70 75
 Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
 80 85 90
 Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
 95 100 105
 Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
 110 115 120
 Gly Ala Gln Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
 125 130 135
 Pro Gln Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

	140		141		150
Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Fr	155		160		165
Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile	170		175		180
Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn	185		190		195
Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala	200		205		210
Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val	215		220		225
Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg	230		235		240
Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His	245		250		255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val	260		265		270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala	275		280		285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn	290		295		300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu	305		310		315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu	320		325		330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys	335		340		345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala	350		355		360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys	365		370		375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val	380		385		390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser	395		400		405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr	410		415		420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Fr	425		430		435

Val Thr Phe Ile	Gly Lys Asn Tyr Arg	Ala Asp Arg Gln Cys Gln	445	450
Leu Thr Phe Gly	Pro Asp Ser Asn His	Cys Ile Gln Leu Pz	455	465
Pro Cys Ala Ala	Leu Trp Cys Ser Gly	His Leu Asn Gly His Ala	470	480
Met Cys Gln Thr	Lys His Ser Pro Trp	Ala Asp Gly Thr Pro Cys	485	495
Gly Pro Ala Gln	Ala Cys Met Gly Gly	Arg Cys Leu His Met Asp	500	510
Gln Leu Gln Asp	Phe Asn Ile Pro Gln	Ala Gly Gly Trp Gly Pro	515	525
Trp Gly Pro Trp	Gly Asp Cys Ser Arg	Thr Cys Gly Gly Gly Val	530	540
Gln Phe Ser Ser	Arg Asp Cys Thr Arg	Pro Val Pro Arg Asn Gly	545	555
Gly Lys Tyr Cys	Glu Gly Arg Arg Thr	Arg Phe Arg Ser Cys Asn	560	570
Thr Glu Asp Cys	Pro Thr Gly Ser Ala	Leu Thr Phe Arg Glu Glu	575	585
Gln Cys Ala Ala	Tyr Asn His Arg Thr	Asp Leu Phe Lys Ser Phe	590	600
Pro Gly Pro Met	Asp Trp Val Pro Arg	Tyr Thr Gly Val Ala Pro	605	615
Gln Asp Gln Cys	Lys Leu Thr Cys Gln	Ala Arg Ala Leu Gly Tyr	620	630
Tyr Tyr Val Leu	Glu Pro Arg Val Val	Asp Gly Thr Pro Cys Ser	635	645
Pro Asp Ser Ser	Ser Val Cys Val Gln	Gly Arg Cys Ile His Ala	650	660
Gly Cys Asp Arg	Ile Ile Gly Ser Lys	Lys Lys Phe Asp Lys Cys	665	675
Met Val Cys Gly	Gly Asp Gly Ser Gly	Cys Ser Lys Gln Ser Gly	680	690
Ser Phe Arg Lys	Phe Arg Tyr Gly Tyr	Asn Asn Val Val Thr Ile	695	705
Pro Ala Gly Ala	Thr His Ile Leu Val	Arg Gln Gln Gly Asn Pro	710	720
Gly His Arg Ser	Ile Tyr Leu Ala Leu	Lys Leu Pro Arg Gly Ser		

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu	Met Pro Ser Pro Thr Asp	
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu	Arg Tyr Ser Gly Ala Thr	
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His	Gly Pro Leu Ala Gln Pro	
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly	Asn Pro Gln Asp Thr Arg	
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg	Pro Thr Pro Ser Thr Pro	
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His	Arg Arg Ala Gln Ile Leu	
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Gln Ile Leu Arg Arg Arg Pro Trp Ala	Gly Arg Lys	
830	835	

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 <112> DNA
 <113> Artificial

<120>
 <121> Artificial Sequence
 <122> 1-23
 <123> Synthetic construct.

<100> 318
 ccctgaagct gccagatgcc tcc 23

<110> 319
 <111> 24
 <112> DNA
 <113> Artificial

<120>
 <121> Artificial Sequence
 <122> 1-24
 <123> Synthetic construct.

<100> 319
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<110> 320
 <111> 43
 <112> DNA
 <113> Artificial

<120>
 <121> Artificial Sequence
 <122> 1-43
 <123> Synthetic construct.

<400> 320

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<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

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ctaaatgcag aagcttttaa atccaaagaa atatgtaaat cacttaagat 150
ttgtggactg gtgttttgta tcttggcctt aactctaat gtctgtttt 200
gggggagcaa gcacttcttg cgggaggtac ccaaaaaagc ctatgcatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatatccag aagcggaaat ggcactgatg 350
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ctctctttga acagtcagtg atttgggtcc cagcagaaaa ccttattgaa 550
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gaacatgtat tggatcaatc ccactctaat atcagttctt gacttacaag 650
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<210> 322

<211> 317
 <212> PBT
 <213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe
				80					85					90
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe
				95					100					105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys
				110					115					120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro
				125					130					135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe
				140					145					150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn
				155					160					165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn
				170					175					180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu
				185					190					195
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala
				200					205					210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro
				215					220					225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu
				230					235					240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe
				245					250					255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg
				260					265					270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Phe Leu Leu Gly
285 290 295

Tyr Tyr Phe Tyr Phe Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Phe Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ataccagaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
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 ggctgtttat gaaaaaaaaa aaaa 1174

(210): 324
 (211): 239
 (212): PRT
 (213): Homo sapiens

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 20 25 30
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
 35 40 45
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
 50 55 60
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
 80 85 90
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
 110 115 120
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
 125 130 135
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
 140 145 150
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
 155 160 165
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
 170 175 180
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
 185 190 195
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
 200 205 210
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
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<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

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 aaccccgta cctcctgtgt ccagtaacga gggtcttgga ggagctggct 250
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 cccctcttc ctctactca ataaaccaa tcttatctc tttccagct 1250

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 aaaaaatcag ccagtcctgg tggcatacac ctgtagtccc agcattccgg 1950
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<310> 326
 <311> 261
 <312> PRT
 <313> Homo sapiens

<400> 326
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 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe	Ala Leu Lys Cys Ile Arg	
95	100	105
Ile Gly Ser Met Thr Asp Ser Ala Lys	Ala Asn Met Thr Leu Thr	
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly	Leu Cys Ala Ile Ala Gly	
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val	Thr Asn Phe Trp Met Ser	
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly	Gly Met Val Gln Thr Val	
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala	Leu Phe Val Gly Trp Val	
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly	Val Met Met Cys Ile Ala	
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr	Asn Tyr Lys Ala Val Ser	
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala	Tyr Lys Pro Gly Gly Phe	
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn	Thr Lys Asn Lys Lys Ile	
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp	Glu Val Gln Ser Tyr Pro	
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Ser Lys His Asp Tyr Val		
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<210> 3.7

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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 tgttttggtt ttcatctgtc taccaaaaaa acaacaacaa aaaaaattgt 1750
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Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
 215 220 225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
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 gacagcttcc atcggcaaca gcctcgtggt ggcacaggtg gtgtgggagg 150
 gccctgtggat gtctcgggtg gtgcagagca caggccagat gcagtgcag 200
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 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggtct 850
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 cctctgttcc ctccctcctg ataagacgtc caccctccag ggcaggtcc 1200
 acctatata gaccctgggc ccacactcca agactgcacc cttctgcctt 1250

ccccccctgg cttccacccc ttccacaccca ccttttttccc aaataaaagca 1300

tggtttgttgc gttccc 1415

<210> 330

<211> 320

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
	20								25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
			35						40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
			50						55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
			65						70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
			80						85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
			95						100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
			110						115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
			125						130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
			140						145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
			155						160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
			170						175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
			185						190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
			200						205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
			215						220

<210> 331

<211> 3160

<212> TNA

<211> Homo sapiens

<400> 111

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gtaaaggcaa tggcatitta tcccttgcaa attgctgggc tggttcttgg 150
gttctcttgc atggtgggga ctcttgccac aacccctctg cctcagtggt 200
agagtatcag ctittgttgg cagcaacatt attgtctttg agaggctctg 250
ggcagggttc tggatgaatt gcacccgaca agccagggtc cggtttgaat 300
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cgaaagtttc aatttgttac tggtggtagg aatgaaaatg acttaacttg 950
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cgtctctcca attttccatc tataaattca agtataccca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgacct catgtattat 1100
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acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 ctcaagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 ggaagtatcc agtgggtggc atccctgccc ccatacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccca 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 gaattctcca tggacataga gagaaaggaa tcatattctc atcatcatct 350
 tcatatccc aggtctgac taagtttctt taagttttac tgaatgtctg 400
 atcttggac atagccagat taagatcat cttagctcaa tggagaaatt 450

ttttttata cccctacaaa cccatgcctc actaacagac cagcattttt 500

ttttttacac gtcataaaa caataatctc ccaga 135

<211> 334

<211> 85

<212> FRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Ile Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 242

<212> INA

<213> Homo sapiens

<400> 335

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tggcctgcac cgggctggcg ctgctcctgc tctgtgtctg gggccccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaaa gagaagcacc 200

tgttccaaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tcttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggctg agcagtggtc ccagcagttt cctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaatiggtc ccgagagccc ctacggcttt aggcattggg ccagcgtcaa 500

ctacgatgac tactaandat gacttgcac acgctgtaca agaaagcaat 550

gagatcttc tctatgatac tctaaagcc ttacactact tggattctga 600

tttttttat tttagaatat cttttttttaa tactttttt: gataaaaaaa 650

gaattgtta aaaaatagat gtaaatgoot ttatataat catgggaatg 700

ttttttttaa aaaaatagaa ataaagcaat ttgtttaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15

Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30

Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45

Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60

She Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75

Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90

Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105

Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120

Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135

Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

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tgaaggggtg ggtgatgagg tgaccttctt tttctcggtg cttgcttgc 150

ttctgttact ggaccttacc tgggtctcaa ggcacacccc tgaggggcgg 200

gagcagatcc cagagatctc aggcacccca aggcacatcc aggcctaggg 250

attatagga attatagga gattgagagg gtagggccca ggggacagaa 300
 ccccccactt tttttacaga ggtcaagctg cacagccaga gcccagccag 350
 tttttacaa caacacccgc agcccaggac tcccgcacag agcccctcct 400
 gttacggctg aaattctctc atgattcaga gcaggttggc agggcctggc 450
 cccacgacac ctttggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcaggtgc gactcatctc ccaagggcag ctgctaggcg acgacaccca 550
 aacccctggc agccttcacc tccctcccaa ctgggttctc cactgcccag 600
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 aaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
 1 5 10 15

Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
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 atgacaaaagg cgtactcatc ctatttggtc agcagcttct ttgcctaaa 200
 tcaggccagg ctcatcagtc gctctgaactt gcccagata ctgcagctga 250

aggaattgga tgggttttag gattactcgc tgaatgactg gctgtacctg 300
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 tggagatttt tactatgggc tcttcacat caacacccac tactggtaca 400
 acgattataa agttactcg gaagaccttt cccacgtaga ctgtcaagat 450
 ctgtcgaatc ccaacctctt tgcaggatc cactggcgaa aaaggattct 500
 gtccgnaaca cyggggatga acaactgggt agaattggagg ttgcactgtt 550
 cagggcggcc actctctac tgggtgacg gatggcgctt gagatgaaac 600
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 ggattcttca tttctcttc ctactgctc caattcatgt tattttcttc 700
 ccttcacatt tacaactaaa actgaccaga gcccacggaa taaatggttt 750
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<210> 340
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 340
 Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
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 20 25 30
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
 35 40 45
 Asp Trp Leu Cys Leu Ala Phe Val Gln Ser Lys Phe Asn Ile Ser
 50 55 60
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
 65 70 75
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
 80 85 90
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
 95 100 105
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
 110 115 120
 Arg Gly Met Asn Asn Trp Val Gln Trp Arg Leu His Cys Ser Gly
 125 130 135
 Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341
 <211> 23
 <212> RNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 341
 ...ttctaaagg atgacaaagg cgc 23

<210> 342
 <211> 19
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-19
 <223> Synthetic construct.

<400> 342
 ...ggtcaacagc ttctctgccc taaatcagg 29

<210> 343
 <211> 14
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-14
 <223> Synthetic construct.

<400> 343
 ...tctcaggcg gcatactgtc agcc 24

<210> 344
 <211> 14
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-14
 <223> Synthetic construct.

<400> 344
 ...ctggatgctt gcaagaaggt tggg 24

<210> 345
 <211> 45
 <212> RNA
 <213> Artificial

<210>
 <211> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 345
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<210> 346
 <211> 2575
 <212> DNA
 <213> Homo sapiens

<400> 346
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 actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
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 aaggagaaaa cgggggtaaa gggagggaag caattcaatt tgaagtcctt 200
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 ggggtgaaac ttgggtcttg tggttttctg attgtaagtg gaagcagggt 300
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 ctccagttcc tctgtctgt cctgatgtg gcatggttc tgatgatggt 550
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 gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950
 aaccatctga acccaggccc agtttctctg gaaagctcca caaacctgga 2000
 ctgggctct gtgcagactg ccaggccagaa ggggacatcc tgggtgtccc 2050
 catggtgttg gctccttgca gtgacagccg gcagcaacag taactgcagc 2100
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 ggccatccac cagcagcact gggacttcca ggagaatggg atgattgtcc 2250
 acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300
 gatttgtacc tgcgtccgtg tgatggaaaa gccccgcagc agtggccatt 2350
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 aagagaattt tggccatcaa aatccagctc caagtgaacg taagagcttt 2450
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Latticarta actinoptera acta 2175

<210> 347

<211> 639

<212> FRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30

Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45

Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60

Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75

Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90

Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105

Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120

Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135

Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150

Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165

Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180

Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195

Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210

Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225

Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240

Ala	Leu	Ser	Gln	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

235

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu	Gly
260		265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala	His
275		280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg	Ile
290		295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val	Ile
305		310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln	Arg
320		325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu	Pro
335		340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile	Arg
350		355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His	Tyr
365		370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg	Gly
380		385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly	Gly
395		400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr	Gln
410		415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu	Arg
425		430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys	Glu
440		445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys	Ala
455		460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg	Leu
470		475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro	Glu
485		490	495
Leu Tyr Pro Ser	Gln Pro Arg Pro Ser	Phe Ser Gly Lys Leu	His
500		505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly	Asp
515		520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser	Arg
530		535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Gln Ile His	Phe

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val		
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln		
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser		
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu		
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe		
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 548
 <211> 13
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 548
 -gagaggtgg tggccatgga cag 23

<210> 549
 <211> 14
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 549
 -ctgtcac'gc aaggagccaa cacc 24

<210> 550
 <211> 45
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-45
 <223> Synthetic construct.

<400> 550
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<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
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tccctctctg ggcactgctg ttgatgcacc tcccacccc tgctcaggga 150
tcttcactct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtg 200
caggggaggc cctcggccc cactcactgt gtgctgtgtg gagcgagac 250
ctccacaaag ccgatctct cgggtccaa gatcagctcg gaaagtctg 300
cctggcactg cacccccagc caccacata ggttttgagg agggggccgc 350
ctatcccaa taccctggg ctatcgtgtg gggccccacc gtgtctcgag 400
aggatggagg ggaacccaac tctgccaac ccggatttct ggaatatgt 450
tttgagccc ctcatgggt cgaacccca caccccaact cagactccat 500
gagaggtgat ggagatggg ctatccttg agaggcaat gcaacctgc 550
ggcatctct gttcggggg cgtggggaag gtctggaccc ccagctctat 600
gtcacaatta ccatctccat catcattgt ctctgggcca ctggcatcat 650
cttcaagtto tctggggacc gacgccaga gagacgcaga cctcaggga 700
agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750
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caccctgac catgaggagc ccgagggggg acccggcct gggatgcacc 850
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 tcaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> FRT

<213> Homo sapiens

<400> 352

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 10 19

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
				20					35					30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<10> 353

<11> 480

<12> DNA

<13> Homo sapiens

<400> 353

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agggcagcat ggcactctt ctgactctc atgtggagat gctctctgtc 100

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 cgtgcccacc ctgtgaaacg agccggccga gctgcccctg ggagaaggcc 200
 ccgtggagag caccagcccc ggccggggagc ccgtggacac cggcccccca 250
 acccccaccg tcggccacgg acccgaggac agcaccgggc aggagcggct 300
 ggaccagggc ggccgctcgc tggggcccg cgtatcgcg gccatcgtga 350
 tggccgcctt gctggccacc tggctggtgc tggcgtcgt ggtcgtcgcg 400
 ctgagaaaagt tttctgcctc ctgaagcgaa taaaggggac cggcccgccc 450
 cggcccgac tcggcaaaaa aaaaaaaaaa 480

<110> 354
 <111> 121
 <112> PRT
 <113> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ter

<110> 355
 <111> 2134
 <112> DNA
 <113> Homo sapiens

<400> 355
 cggccttgggt tggctgcggc ctgaagggtg tggcccgagc agcctcgtta 50
 attggccggg ggagggaggg caccggcatg gacatgtgca tctgctggtt 100

atttctatg agcagctatg cccacggctg tttacatga cccatcaat 150
 tctcaaaa gttctcttc taccgcaac atgtgaatt caagtcccg 200
 tgaatgggg acatcccccgt gtcaggggg ctctcacag actggagaga 250
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 agaagctga ccaagtggcg acagcigtgt accagatgat ggatcagctg 350
 taccagggg agatgtactt ccccggtat tccccaaag agatcggaa 400
 tatcttcgg gacacqctgc acctcatca gaacgcata atcgaaagg 450
 acctgcacc aggcacctgg agagtaggg agctctcag ggaggagcc 500
 agctagcac ctgaaggatc aatgcacac ccccggggg acctcccta 550
 agtagcccc agaggcgctg agagtgttg caccgcctc cctgaagtt 600
 tgcacatct caccgtgggg gtaacctg ggacccttc cctcggggc 650
 atgacacac atacatgaaa accaggccgc atgactgtc agcacgctg 700
 tggcatcttc cagtaacgag ccatctctg caacaactgc acagactgc 750
 acgtgcctg ctctggctat aactgcaggt agggctcagg catcacccc 800
 accgtgcca ggccctact gtccctgggg tcccaggctc tcttagagg 850
 aggcacccg ccttcacct ggctgtcct gggtagggg gggccgtggg 900
 ttcajgggg caccacttc aagctgtgt cccacaggtc ctggggag 950
 tggagtcat ctgtccagg cctcctgaac tacataaata actggcaca 1000
 gtaagtccc tctcaaac aacacaggca gtgtgtgtat gtgagcact 1050
 cgtgggtgag tatgtgtgg ccacaggctg gctcctcag ctccacgct 1100
 ctagaggggg tccgaggag gtggaacctc aaccagctc tgcgcaggag 1150
 ggggtgcag tcttttctc cctcaagggt ctccgacct cagctggagg 1200
 cgggcattt tctaaaggg tcccatagg gtctgggttc accccatccc 1250
 aggtctgtg tcagagctg agagggttc ctacgatgt taggggtgc 1300
 ccattggagg gctgactgc ccacattgc ttccagacag gacacgagca 1350
 taaggtcagg cggccctgac ctgacttca gggggagggg gtaaaaggag 1400
 agaggaggg ggctagggg tctctagat cagtggggg actgcaggtg 1450
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<210> 356
<211> 157
<212> PRT
<213> Homo sapiens
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Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala	
1				5						10				15	
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser	
				20					25					30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	
				35					40					45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	
				50					55					60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	
				65					70					75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	
				80					85					90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	
				95					100					105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	
				110					115					120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln	
				125					130					135	
Leu	Ser	Arg	Gln	Gly	Ile	Ser	Ile	Ala	Pro	Gln	Gly	Ser	Met	Pro	

• • •

[illegible]

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
1				5					10					15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
				20					25					30
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35					40					45
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50					55					60
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65					70					75
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80					85					90
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95					100					105
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110					115					120
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125					130					135
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140					145					150
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155					160					165
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Tyr	Ala	Ala	Lys	Leu	Ile	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195

11- Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser		
	210	215
12- Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr		
	215	225
13- Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val		
	230	240
14- Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly		
	245	255
15- Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys		
	260	270
16- Val Glu Leu		

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 tagcagtgcc ccatctcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tagcagtggtg gatacaactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aactctctct ctgg 24

<210> 362

1111
 1112 DNA
 1113 Artificial

1114 Artificial Sequence
 1115 1-50
 1116 Synthetic construct.

1400> 362
 1401 atgacagga ggtgcatttg ggatcaccac tgattctag gttctgacac 50

1410> 363
 1411 1777
 1412 DNA
 1413 Homo sapiens

1400> 363
 1401 gtagagccgc ggcctggacc ggagtgggga ggcggggctg gaggtgcac 10
 1402 cggcgccggg tggcggaag atcagaagcc tcttccccc gccgagccaa 100
 1403 cctcagcggg gaccggggct cagggacggc ggcggcgccg cggcgactgc 150
 1404 agtggctgga ccatggcagc gtcggccgga gccggggcgg tgattgcagc 200
 1405 cccagacagc cggcgctgga tgtggtcggg gctggcgccg gcgcttgggc 250
 1406 tcttgacagc tggagtatca gccttggag tatataccc aaaagaaatc 300
 1407 ttctgtgcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
 1408 tagtaagact ggcgggttga cctcagcttc ctggagcttc cagccagagg 400
 1409 gggccgacac tactgtgtcg tttttccact acctccaaagg gcaagtgtac 450
 1410 cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
 1411 tgacaagaaa gatgcacaa tcaacataga aaatatgcag ttatatac 550
 1412 atggcaccta tatctgtgat gtcacaaacc ctctgacat cgttgtccac 600
 1413 cctggacaca ttaggcctca tgcctgagaa aaagagaatt tgcctgtgtt 650
 1414 tccagtttgg gtagtggcgg ccatagttac tgcctgtggt ctaggctctc 700
 1415 ctctgtctat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
 1416 aaacgggatt acaactggct cagtaacaca gagagtttgt caccagttac 800
 1417 ccaggctcct cagaagtcac cctccgacac taagggtctt gtaagaaatc 850
 1418 tgcctctctg atctcaccag ggcacagtc tatatgcaca gttagaccac 900
 1419 tcttctctac atcacaatga caagattaac aactcagct ctctgtctca 950
 1420 tctctctctc ccaaaatatt aaagaaatcc ctgagacata tctctgacaa 1000

aaatgaaac caaatgaaac tctctttaa aaatgaaac caaatgaaac 1150
 atgagactt ggagaccaa gcaacaca atacaagtgt atcaataga 1160
 aagagaaaag atgtgtacaa aggatatgta taatattat atttagtca 1170
 atgtatatga ggagcaagtgt ttgcatgat gaaagatggt atgattctac 1200
 atatgtaccc attgtcttgc tgtttttgta ctctcttttc aggtcattta 1250
 caattgggag atttcagaaa catctctttc accatcattt agaaatcttt 1300
 tgccttaatg gagacaaatag cagatcctgt agtatttcca gtagacatga 1350
 ccttttaate taagggttta agactgatta gtcttagcat ttactgtagt 1400
 tggaggtatg agatgctatg atggaagcat acccagggtg gccttttagca 1450
 cagtatcagt accattttatt tctctgcgcg ttttaaaaaa taccatttga 1500
 ctatgccact tgaaaacaat ttgagaagtt ttttgaagt tttctcact 1550
 aaaatatggg gcaattgtta gccttacctg ttgtgtagac ttactttaag 1600
 ttgtcacctt tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaaq gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttttaa 1750
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
 <211> 269
 <212> PET
 <213> Homo sapiens

<400> 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
 95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile	110	115	120
Asp Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys	125	130	135
Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile	140	145	150
Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val	155	160	165
Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr	170	175	180
Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn	185	190	195
Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser	200	205	210
Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly	215	220	225
Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile	230	235	240
Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile	245	250	255
Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn	260	265	

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
 gccggctgtg cagagacggc atgtacgggc tectgtcagg agtgactgcc 50
 cgggctgccg cccccggggg cttgggectca agctgaggac gacgcggggg 100
 ccacacagcg gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 aggggcggcg cccggggcca gtcggcgcg gcccccgaac ctgaggcctc 250
 ggcctctggc gagccggcac aggagcagtc cctcgcccg tggtctccgc 300
 agacccgggc gccgcctgc tccaggtgtc tcgcacagac cctcgagacc 350
 acccgcgacc tctgtcacag gatcaaggat gagggtggcg caacgggcat 400
 atgttttca cttctgttac atgacagag actctgtca caagttttc 450
 attatctga tcttgacac cctgtacac ctacacaga caacgtttat 500

tttttttt gaattagaaa aattttcaac atgatttatt tttttttt 550
 tttttttt gggaaaatgg attttgatat tccagtacaa tttttgtt 600
 tttttttt agaaaaagaa tatgaaggtg aaaaggtttt tttttttt 650
 attttttt tttccattt aattggaatt agtcattatg aaaaggaat 700
 attttggtg aaagaagaga aagcttataa agccttgaag atgatgaaa 750
 aaaaattg atttgagcaa gaaaaagaag gcaaaaagtaa tgaagaaga 800
 tttttttt aattttaaac agagcaggag aatgaagcaa aatgcaggaa 850
 tttttttt ggcaagaaaa agaattgatt tgaacaaggc gaatttat 900
 tttttttt gtttgaaaat tcaattgaat cctaagatt atttataat 950
 gatctttgt ttttcaaac tggtagtcag tttttgtatt caacttttgg 1000
 ctatcccta ctggcagcca tagtagagag agcttcagaa tgtaatatt 1050
 tggactatat gcagaaaaata ttccatgaat tggatatgt gacgaatgtg 1100
 caggaagaaa acgagcaggt gatttacaat agagcaaggt aatgaatac 1150
 cttctgtgt gtctagctat atgcacatt aacactattt tattaattaa 1200
 aagtaaaatt ttctttgttt ccattccaaa atcaactctc cacattttgg 1250
 gagcttttct acatgttgt tttctcatct gtaaagttaa ggaagtataa 1300
 catgtttata aagtaaaaaa a 1321

<110> 366
 <111> 373
 <112> PRT
 <113> Homo sapiens

<400> 366
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
 1 5 10 15
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Gln
 65 70 75
 Ala Ser Pro Leu Ala Gln Pro Pro Gln Gln Gln Ser Leu Ala Pro
 80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	105	106
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	110	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	125	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	140	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	155	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	170	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	185	195
Phe	Pro	Glu	Lys	Gln	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	200	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	215	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	230	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	245	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	260	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	275	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	290	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	305	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	320	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	335	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	350	360
Gln	Glu	Glu	Asn	Gln	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			365	370

<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
TGTAAAAGAA GTCTGGTCAG AAGGTTTAGG 30

<210> 368
<211> 15
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
GATTGGGTTT CATTCTCTGT CTCTG 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
GAAACCTCAG AACAATCAT TTGCACC 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
TCTCAACCAT GGTTCCTCTT GCCAAATTGT GCGAAGCAGG G 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
TGTCACTAT ACAAATCTA TCAAGTCGCA TCAATCTATA CATACTCTG 10

aattttagt ctatcttggg ggaagaaga agagatgga caatccagcg 170
 ctggggaag cgggttgctc ctgctcttgc tgatggcggt agcagcgccc 180
 cgtccagccc agggcagggc ctgcccggcc gggactggcg cgcgaggggc 200
 tctggcgaaa cgtcgagagg ggcaggccctg tggcacggcg ggcctgctgc 250
 tctagcactc atttgagatc gatgacagtg ccaacttcgc gaagcggggc 300
 tctctgctct ggaaccagca ggatggtaac ttgtccctgt cacaagcgga 350
 cctcagcgag gaggagcggg gcggactcgc ggtatgggca ggcctgaatg 400
 gcttgtaacg ggcccggaac caagggcgac cgggggcctt ggtatggctg 450
 gaagctggcg gctatgtctc ctcttttgc cctgctgct ccttggctga 500
 ctgcacctg tcggaccagc tgacctca cgtggatgcg ccggccaacg 550
 tggggggcgt gtgggtggcg accaccccg ggggtcgccg gggccatgag 600
 gtgaggagc tggacctgga gctgttcaac acctcggcgc agctgcagcc 650
 ccccaaccac gccccaggcc ctgagacggc ggccttcatt gagcgccctg 700
 agatggaaac ggcccagaag gcccaagaac ccaggagca gaagtccctc 750
 ttgcacaaat actggatgta catcattccc gtctctctgt tctcatgat 800
 gtcaggagcg ccagacacgc ggggcccagg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tctgtgtgc caccctccct gtaagtctat 900
 ctaaaaacat cgaagataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttcacgc agccaaaagc aactgttctt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaatc actgctcact tgatacgtta ttcagaaac 1050
 caaggaaagg ctgtcccat cctcatgtgg ctgtgtggag ctcaactgtg 1100
 ttgtgtgaca gtttattaaa ctgtccccc gatcgacacg caaaaaaaaa 1150

<J10> 372

<J11> 269

<J12> PRT

<J13> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40					45

Ser	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				80				85						90	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				85				90						95	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				90				95						90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95				100						105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110				115						120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125				130						135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140				145						150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155				160						165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170				175						180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185				190						195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200				205						210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215				220						225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230				235						240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245				250						255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260				265							

<110> 373

<111> 1706

<112> DNA

<113> Homo sapiens

<400> 373

ggagcgctgc tggaaaccga gonggagccg gacccacacc ggggaggggtg 50

gactgggggc ctggagccgg acgtgtccgg gggtccccg cagaccgggg 100

caccaggtcg tccgggggac caccatgctg gtgactgctt accttgcttt 150

tgtagaccta ctgctctctt gactgggctt agaaatctca agatgcgggg 200

ttaattttac tggaaaggac taaagaatc cctccttctc tgggttttca 286
 ttaattttat atcaggtata cttctctggc ctggcagctg attgctttca 300
 ttaattttac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
 aaatttccat cctctatgtc tgttgccttg cctctacagt cctctttgac 400
 ctatggcct cctccttctg ggattggctg ggtcgcaaga attctttctg 450
 cctctttctc ctgaattact cactatgtg cttaaccaaa ctctctcaag 500
 actactttgt gctgttagtg gggcgagcac ttggtgggtg gtcacagac 550
 ctctctttct cagccttoga ggcctggat atccatgagc aggtgcaacg 600
 caatgaattc cctgtgagt ggtaccagc tacccttctg agagctgct 650
 tctggaacca tgtgtgggt gtagtggag gttggcagc tgaggtgta 700
 gacagctgga taggctggg gcctgtagc cctttgttg ctgcacccc 750
 tctctgggt ctggaaggg ccttggcctc tggaaactg gggagaaat 800
 atgacgggca gctgtcctc tcaaggacct gtgtggagg cctgcctgc 850
 cctcgtggg acgcggcgt gctgtgtg ggcacatc aagctctatt 900
 tgagagtgt atcttcctt ttgtctctc ctggacact gtgtggac 950
 caaacgggc cctctgggc attatctct cagcttcat ggcagcagc 1000
 ctgcttggc cttcctgtc ccgtatgac acctcaaga ggtaccact 1050
 tcaacccatg caactgtgt ccttgtgt gctcctgtc gtctctctc 1100
 tcttcctgtt gactttctc accagccag gacaggagag tccggtggag 1150
 tcttcctag cctttctact tattgattg gcttgtggat tatacttcc 1200
 cagcatgagc tctctacgga gaaaggtgat cctgagaca ggcaggtct 1250
 gtgtactcaa ctggttcgg gtaactctc actcactggc ttgctaggg 1300
 ctccttctc tccatgacg tgatcgaaa acaggaactc ggaatatgtt 1350
 cagcatctgc tctgtgtca tgggatggc tctgtggca gtggtgggac 1400
 tcttcacgt ggtaaggcat gatgtgagc tggggtaac ttcactact 1450
 gaggagcct atgcctctg gctgtaacc cactccagga caagatagt 1500
 ggcacagact cttgaattc agctatcgg gattgtaacg atctctctgt 1550
 gctgaattt gtgactctc tgtgtttct cctgcattg ctttgtgtt 1600
 gctgaactt gctggtgtg atgactga aagagctcc caaaatttc 1650

...ctccatita gaaatgac accttttaatt gatcaaaaaa 1730

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Met Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
5 10 15

Pro Leu Gly Leu Gln Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Gln His Val Glu Arg His Asp Phe Pro Ala Gln
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Arg Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile	245	250	255
Ala Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp	260	265	270
Thr Arg Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe	275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg	290	295	300
Ala Ala Thr Ser Lys Arg Tyr His Leu Glu Pro Met His Leu Leu	305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr	320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile	335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser	350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala	365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys	380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr	395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu	410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu	425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu	440	445	450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

gacacgcgcg ggggggcgcg gagaggaaac ggggcgcgcg gccgggcgcg 50

gacctggaga tggccccgcg cggcgcgggc tgggtgtgtc tgggtgtgtg 100

ggtccccgcg tgggtgcgcg cccacggctt ccgtatccat gattatttgt 150

actttcaatt actcaattct ggggacattc tatacatcct caaagacada 200

actcaaaaat acttttgttg tatctttcac aaaggttatg aaagatttca 250

atgtatgaa ggtgaacatc cagagagcctc agaggaatc agaaaagggtt 300
 tcttcattcc ggcacagatt gctctgctgg agagggggag ctgctccttc 350
 ctctcaaaa ctgggttgt ccaggagcac ggcggggggg cgttgatcat 400
 ctctgacaa gcatttgaca atgacagctt ctacgtggag atgatccagg 450
 ctactacca ggcacagct gacatcccg cctcttctct gctcggccga 500
 ctacgctaca tgatcccg ctctctggaa cagcatgggc tgcctgggc 550
 ctctatttc atcccgatc atgtccacag cctccccc tttgagctgc 600
 tccaaccgct ctggaccttc tggtagaaga gtttgctcca ccttcagcc 650
 ataagtgaat ctgagctggg aaggggaaa caggaattt tgcacttgg 700
 aatttgaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttggcggtt gctaggtga aagggagcc aaaccactgg ccttccttc 800
 cccaggccc ccaaggtgt ctcatgtac aagaagaggc aagagacagg 850
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 ccttgagagc catctgtgac ctgtcacact cacttggtc cagcctccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 376
 Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
 1 5 10 15
 Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
 20 25 30
 Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
 35 40 45
 Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
 50 55 60
 Gln Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
 65 70 75
 Gln Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
 80 85 90

Met	Ala	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25						30
His	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35					40						45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50					55						60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65					70						75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80					85						90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95					100						105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
			110					115						

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 tttccctccac tgcctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
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<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<12> Synthetic construct.

<11> 761

cttaccaga tgytcaata actaatatg aaatgcca tctc 45

<11> 382

<11> 764

<21> DNA

<21> Homo sapiens

<400> 382

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gggattgttg aqqtgcccq gcacaaccag acgcccagtc acaggcgaga 100
gacctgggat gcaccugcca gaggccatgc tctgtgtgt cagctttgac 150
ctcttggggg cccccacctg ggcagggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga caatgaaatc acaggggtgc 250
gggtatctgt aggttttttc ctgggtgaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcetta ggtgggaata cccaggaagt 350
cactctgagc ccaggcgcat acatcacaaa agtctttgtc gctttccaag 400
ctttctctcc gggatatggt atgtacacca gcaaggacag ctatttttat 450
tttgaaaagg ttgttgcca gatctctctt gctacccca gccaagaggg 500
gcaggtgctg gtggccatct atggccagta tcaactcctt ggcataaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650
gglatggggc cctcccaqct gaggccatct gtgtgggtgt ggtgatggt 700
actggagtaa ctgagtcggg acgtggaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> FRT

<213> Homo sapiens

<400> 383

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Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
			20						25					30
Gly	Lys	Tyr	Ile	Ser	Thr	Thr	Gln	Asp	Tyr	Asp	His	Glu	Ile	Thr
			35						40					45

Ala Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
 15 35 60
 Leu Leu Gly Asp Ser Tyr Asp Val Lys Leu Gly Ala Leu Gly
 65 90
 Thr Gln Gln Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
 95 120
 Arg Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
 95 100 105
 Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
 110 115 120
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
 125 130 135
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
 140 145 150
 Phe Thr Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
 155 160 165
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
 170 175

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
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 atacagatgt ggcagctcag gtagecccaa attgcctgga agaatacacc 150
 atgttttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca ccccccaaaa aaactgtaaa gatgcacaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgcg gcaaatgcgg 300
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 atgttccaaa atcgggtccat ctcccaagga gtccaatttt tottcttggg 400
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aatataaa ttatagtaga taatataa tataatataa gttatataa 750
 attatgtaaa tggatataaa agtatataa aaataataa taataattt 750
 aatataaa aatagatataa atataataa atagatataa aatataaa 800
 aatataaa gaaaatgatt ttataggaat agtatataa aatagatga 850
 attatgtaaa aatagataa taatatttt ttataataa attatagatt 900
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 ggtatataa attatgataa attatgtaa ggtatataa ggtatgtaa 1050
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 aatataaa ggtatgtaa taatataa aatataaa attatgtaa 1150
 attatgtaaa aatagataa attatgtaa ttatagatt ggtatgtaa 1200
 aatataaa attatgtaa ggtatataa ggtatataa ggtatataa 1250
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tttttttt gttttttt aaaaaaaa tttttttt tttttttt 2150
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<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
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 1 5 10 15
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Gln Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Gln Leu

210	205	110
Pro Leu Glu His Asn Gln Ile Ser Lys Leu Asn Leu Ala Leu Phe	215	125
Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys	230	240
Pro Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu	245	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly	260	270
Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu	275	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser	290	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu	305	315
Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe	320	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu	335	345
Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile	350	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu	365	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu	380	390
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly	395	405
Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile	410	420
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu	425	435
Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys	440	450
Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys	455	465
Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr	470	480
Val Asp Tyr Lys Lys Thr Asn Thr Gln Thr Ser His Met Leu Leu	485	495

Ala Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510

Lys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 386

ctggggtctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 387

gtcccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 388

gctgaattta catttacggt ctaactccct gagaaccatc cctgtcgc 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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tttaactgtcc tttaaatatc tcaagatcca gacttttcag tgcacattca 100

gggatctcaa agataatgat ctgtgttttg cagctatttc agttgtgtgt 150

ctcttaacta ctatcgaagc aagatgaaat gtgttataat tttatgagac 200

aacacacaa tagcagatc atcgaatcc tctgctcct gtttttggc 350
 gcaactcttc tcgtgtgagc tctggctctc tgcctccagt cctggatgag 360
 gagacccaga atcgaattctc acaggcgac cctggaaagt tttgctgttg 380
 taatcttggc ctctatttat gggacagaag cagctgtgag tccaaetggt 400
 ggaattcacc ttcaaaactc aacccctgac ctatatactg ttccctgctcc 420
 atgtttttggc ccttttaggt ccccaactcc atatgaagaa attgtaaaaa 500
 caacctgatt ttagatgttg attatcaatt taaagtatta acgacatctg 550
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 gtatgtttcc tccattttag gaactccactg cagtatacag cacaaccatt 850
 tctgctttta actcttttcc agcatgggtt ccataaaaaa tattataatt 900
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 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttccg 1400
 ctgacaaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr

1

6

10

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 Asn Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
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 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 135
 Ser Gly Ser Ile Arg
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<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<401> 396
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 gggcccagac aaccgggcca tgcctccccc ggtgccaatg cgaggtggag 150
 acctcgggac ttttcgacag ctccagcctg actcgggtgg attgtagcgg 200
 cctggggccc cacatcatgc cgttgcccat cctctggac acagcccaat 250
 tggacctgtc ctccaacogg ctggagatgg tgaatgagtc cgtgtttggg 300
 gggccggggt acacgacgtt ggcctggcctg gatctcagc acaacctgt 350
 caccagcacc tcaccacatg cttctccccc ctttcgctac ctggagtcgc 400
 ttgacctnag ccacaatggc ctgacagccc tgcacagcga gagcttcacc 450
 agctcaccac tgagcgacgt gaaccttgcg cacaaccagc tccgggaggt 500
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 acctctccca caacctcatt caacccctcg tcccccacc cagcagggcc 600
 ggcctccctg cgcctcacc tgcagatcg caatctctt gaacccctt 650

atattacatt: cccaaactctc ttttcttggc cctggagctac ct ttttttg 750
 atgggaaacc tctactgttc atttgctcag gtgccttcgc ggggtggga 750
 ggccttacac acctgtctct ccccaactg cagaggctcc ctgacttggc 800
 gaccagtggc ttccgtgagc taacgggcct gcaggctcct gacctgtcgg 850
 gcaaccccaa gcttaactgg gcaggacctg aggtgttttc aggcctgagc 900
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 gggctgtctc ctccactcc cggcaactga gagcgtcagc gtggggccagg 1000
 atgtgcgggt: cgggpgcctg gtgggggagg ccaactacc cgggagcct 1050
 ggcctcagcc ccaaggtgac cctgcactac gtagacacc ggaactctgc 1100
 tgcacggggc cccacccatc tctgacaaat ggtgtggccc agggccacat 1150
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 tctgccaaca ccagtgggga gccgcaggc ctatgtggca ggcctaccac 1250
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 tgggctgagt gtcccttgg gcccatggc cagtcactca ggggcagtt 1550
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 ctacactgg gttggggctc ccagcactcc aacttgaaa cctaccatt 2050
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 aaaaacaagg tctcccagac ccatgtctat gctctacccc cagggcagca 2250
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 aagctggga tcagtggcca catgggcctc aggggtctgc cccacagaga 2500
 cccacaggg cagtgaagtc tgtcttccc cactgccta gccatcctc 2550
 tatctaacg gtccttgatt taataaacac tataaagggt ttaaaaaaaaa 2600
 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 2639

<210> 397
 <211> 393
 <212> FRT
 <213> Homo sapiens

<400> 397
 Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
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 Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
 20 25 30
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Gln Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

His	Leu	Arg	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser	
				165					165					165	
Leu	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly		
			170					175					180		
Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg			
		185					190					195			
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu	
		200						205					210		
Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe			
		215					220					225			
Leu	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln	
		230						235						240	
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly	
		245						250						255	
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala	
		260						265						270	
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp	
		275						280						285	
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu	
		290						295						300	
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg	
		305						310						315	
Lys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly	
		320						325						330	
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser	
		335						340						345	
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu								
		350													

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctggcagc ccagaccttc acc 23

<210> 398

<211> 23

<212> DNA

<11> Artificial

<22>

<21> Artificial Sequence

<22> 1-23

<23> Synthetic construct.

<400> 399

ggttagtgcc cgaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttactggg caggagctga ggtgttttca ggc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

catgggcag ccacagcttc tctgagatc gatttctccc cagttccct 50

gtgggtctga ggggaccaga aggggtgagct acgttggctt tctggaaggg 100

caggctatat ggtcgaatc cccaaaacaa gttttgacat ttccctgaa 150

atgtcattct ctatctatc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacgggg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccactcg cactcagaat ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatgc cacaaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaattottaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgttgctccc tgggcattt gctaaagctc tatctggaca gggatattta 650

aaactacag accttgacc attatactct ccggaagatc agcagctcg 700

caatttctt tcttctctc aagaaggctc tctgtctctc tcatgctac 750

ctatcatctt attgtgagga ggaacaaatg aaacaaatga gccagattct 800
 gattcatctt gaaagctgg aaactcagga agcagttgtg aaggctttgg 850
 aaactaga cattttcttg caatggatgg agagagaga ataggaggaa 900
 agtattcttg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcattgac cccaaaccac catctcttta ctgtactagt 1000
 ctgttctggg taacagtcta tcttatttat gcattacttg ctctcttgca 1050
 ctattctctt tatgaatccc caatcttaat tgagaccata ctgtgtatag 1100
 atttttgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150
 tatctatttt ttgtatttta atgtatttat ttttttactt ggacatgaaa 1200
 cttaaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
 ctaggggggg tattcatttg tattcaacta aggcacatatt tactcatgct 1350
 gatctctctt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gtittgatgt ggaattgcac atctacotta caattactga 1450
 ccataccacg tagactcccc agtcccataa ttgtgtatct tcagccagg 1500
 aatctacac ggcagagatg tattttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<P10> 402
 <P11> 261
 <P12> PRT
 <P13> Homo sapiens

<400> 402
 Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
 1 5 10 15
 Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
 20 25 30
 Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
 35 40 45
 Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
 50 55 60
 Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
 65 70 75
 Leu Leu Trp Ser Pro Asp Ile Arg Pro Lys Met Lys Ala Ser Ser
 80 85 90

100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260
Ala	Thr	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr				
		45					100									105
			Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	
			110				115								120	
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg		
			125						130					135		
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu		
			140						145					150		
Ala	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys		
			155						160					165		
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe		
			170						175					180		
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser		
			185						190					195		
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu		
			200						205					210		
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys		
			215						220					225		
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln		
			230						235					240		
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln		
			245						250					255		
Trp	Met	Glu	Glu	Thr	Glu											
			260													

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctccctgagggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
 <210> nt aaattcttca tptcaa 26

<211> 435
 <211> 998
 <211> DNA
 <211> Homo sapiens

<400> 435
 ccgttatcgt cttgcgcctac tcttgaatgt ccgtcccgga ggaggaggag 50
 agctctttgc cgtgaccca gagatggccc cgagcgagca aattcctaact 100
 ctccctctgc ggggtacacg tggcctagct agcaaccttt cccctggatc 150
 tcaaaaaaac tgcactccaa atgcaaggag aagcagctct tgcctgggtg 200
 ggagacgggtg caagagaatc tgcctccat aggggaatgg tgcgcacagc 250
 cctaggggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
 caccgcctat ttacacacac gtagtgtatt ctggaggctc aatggtcaca 350
 tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
 tcccttttgg aatcagtc a ttggagggat gatggctggt gttattggcc 450
 agtttttagc caatccaaact gactagtga aggttcagat gcaaatggaa 500
 gcaaaaagga aactgnaagg aaaaccattg cgtttcgtg gtgtacatca 550
 tgcatttgc aaaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
 gctgggtacc caatatacaa agagcagcac tgggtgaatat gggagattta 650
 accacttatg atacaqtgaa acactacttg gtattgaata caccacttga 700
 ggacaatata atgactcagc gtttatcaag tttatgttct ggactggtag 750
 cttcttttct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
 caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
 ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
 gatttttacc atcttgctg agaatgaccc cttggccaat ggtgttctgg 950
 cttactatac aaaaaatcag agagatcagt cgagtcagtc cattttaa 998

<210> 406
 <211> 423
 <212> PRT
 <211> Homo sapiens

<400> 406
 Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
 1 5 10 15

Arg	Ile	Arg	Ala	Ser	Lys	Ile	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
			20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
			35					4					45	
Ala	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
			50						55				60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
			65						70				75	
Leu	Arg	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
			80						85				90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
			95						100				105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
			110						115				120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
			125						130				135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
			140						145				150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
			155						160				165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
			170						175				180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
			185						190				195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
			200						205				210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
			215						220				225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
			230						235				240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
			245						250				255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr
			260						265				270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly
			275						280				285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Ile	Leu	Pro	Ser	Trp	Leu	Arg	Met
			290						295				300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg

Protein: Ser His Val Ser Phe His
310

<210> 310
<211> 1
<212> DNA
<213> Artificial

<220> Artificial Sequence

<223> Synthetic construct.

<210> 407
gagatggc attatcgatct tgcgtactg c 31

<210> 408
<211> 1
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<210> 408
gggaattct taaaatggac tgcctcact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
gggacggctg ggcgggggac ggcggcaggg ttgtggcgca gcagtctcct 50
tctggcgagc ggcctgaag tcggcgctggg cgtttgagga agctgggata 100
cagcatttaa taaaaaatit atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttggcca gaatgtgaat gtattgaactg gagtgagaga 200
agaaatgctg tggcatctgt tctggcaggt atattgtttt ttacaggctg 250
gtgataatg attgatgac ctgttgtgta tccaaagcca gaacagttga 300
aacatgctt tcaacatct gggtgatttt ccacattggc tttcttcatg 350
ataaatgctg tctcaatgc tcaggtaaga ggtgatagct atgaaagcgg 400
tttttagga aaaaaatd atagagttt gcttttccatt ggtttcatgt 450
tcatattga ataatatt gcttccatct ggattctttt tegtgcatat 500
tttctttaa atattatit tttctggg atagctgtgt tttttcaaaa 550

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 601
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 650
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 700
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 750
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 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1150
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<210> 410

<211> 158

<212> PKT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Ile	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Trp	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75

Ser Asn Ala Glu Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
 80 81 82

His Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
 95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
 110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
 125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
 140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
 155

<310> 411
 <311> 20
 <312> DNA
 <313> Artificial

<320>
 <321> Artificial Sequence
 <322> 1-20
 <323> Synthetic construct.

<400> 411
 attgaggaa gctggatac 20

<310> 412
 <311> 20
 <312> DNA
 <313> Artificial

<320>
 <321> Artificial Sequence
 <322> 1-20
 <323> Synthetic construct.

<400> 412
 ccaaaactega gcacctgttc 20

<310> 413
 <311> 40
 <312> DNA
 <313> Artificial

<320>
 <321> Artificial Sequence
 <322> 1-40
 <323> Synthetic construct.

<400> 413
 atggagggt tctatataa ttctatatt cagatgtt 40

<310> 414

11. 1137
11. 1138
11. 1139

11. 1140

atgagggga aatttcttca aagaaagggc agaaacttca aggggcagga 50
agagctgggc aattggcggc cggaaacatt caattctacc ctctggggcc 100
actgcattca gaggaggggc gtctgtgagg caactacccc tccagcaact 150
atgagtgga actgtcagaa gctgggcacg ggtgttggtc acctgggtca 200
gggactacg gcacctgtg gacacctcg ccttctccat cgaagcaggg 250
aattggagc ctgagccct cgggtggaat ctacccccc gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctctct ggccctcact 350
tttgcctatg tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaac atcctgtctg cagctgtgtt ggaagctctt cccaccaagg 450
agatccaggt taaaaagtaa aagtgtggcc tcattcaagc ctgccacagc 500
aactactttg cgtttaaaa ctgcagtgga gcccccacg tegtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gactcctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atgaaacac gggagctgtc 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaatc cgggggggtg actggtgtgt gtggcctctt 750
acgacgatcc agggaccaca atgaacgatg aaacacagaa actcttctct 800
gacttgggga gttctacgc aaaacaactg ggttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtta aagcccttt gaccagtctt 900
taaagaacag cccagacaca aacaaatag agggatggcc agagctgtgt 950
gagatggagg gctgcattgc cccgaagcca ttttagggtg gctgtggctc 1000
ttctcagcc aggggcctga agaactcctt gctgactta ggagtcagag 1050
ccccacagga gctgaggaag aggagcaggg agtgcctggt ggaaggtact 1100
gcaggtcctt gcacgtgtg tcgggcctct cctctctgga aacagaaccc 1150
tcccacagca cactctacc ggaagaccag cctcagagag tctttctgga 1200
aacactgtc tctgagaga atgggtgtct tttctagga actgctgac 1250
atctctctc aggaagaca agctccccc actccccc atttaattt 1300
tatttctct cttttgaaa aaaaaaaa aaaaaa 1347

<210> 415
 <211> 224
 <212> 1RT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<10> 1-21
<11> Synthetic construct.

<400> 416
gacatagca gacatggat g 21

<10> 417
<11> 18
<12> DNA
<13> Artificial

<10>
<11> Artificial Sequence
<12> 1-18
<13> Synthetic construct.

<400> 417
gttggccag agctgctg 18

<10> 418
<11> 26
<12> DNA
<13> Artificial

<10>
<11> Artificial Sequence
<12> 1-26
<13> Synthetic construct.

<400> 418
aagtcacag tgtggccca tcaagc 26

<10> 419
<11> 24
<12> DNA
<13> Artificial

<10>
<11> Artificial Sequence
<12> 1-24
<13> Synthetic construct.

<400> 419
tctgactct aagtcaggca ggag 24

<10> 420
<11> 24
<12> DNA
<13> Artificial

<10>
<11> Artificial Sequence
<12> 1-24
<13> Synthetic construct.

<400> 420
attttttta aagtcagga ttta 24

Official

Official Sequence
1-46
Synthetic construct.

421
gggctcatca agccttgccc agccaactac ttctcc 46

422
421 1701
1701 1701
1701 1701 sapiens

423
423 unsure
424 1728
424 unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tctctgggg atccagaaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacaucaaga gaagcagaga taaatacact 150
cagccacaga gctcgctcgc tctctctctc tctctctcag tctctctctc 200
ctctctctct gctctctcta gtctcttagt cctcaaatc ccagtcctct 250
gcacctcttc ctgggacact atgttcttct ccgctctctc gctggagggtg 300
atttggatcc ttgctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctctta ccttgagigt ggaaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgacctgat 450
ttgctctctc tgcagcccca cggatctgac cagcctggca ccgagccttt 500
ggactgcac aacaatggcc acacagtcca actctctctg cctctctacc 550
tgtatctggg tgaacttccc cgaaaatatg tagctgccc gctccacctg 600
cactgggttc agaaaggatc ccagggggg tcagaacacc agatcaacag 650
tgaagcaca ttgagagaga tccacattgt acattatcac tctatctct 700
atgacactt gactgaggt gctgagagg ctcaggcctt ggtctctct 750
gcatctca ttgagtggt ttgagctaa catatagctt atgaacact 800
tctatctca tctatgaa tctatctaa atctatggt acctagctt 850

ctacttttaa cctaagagag ctgcttctta aacatcttca gcttacttt 9 0
 cgtatcaatg gctcgtctca aactccctct tctaccaga gtgtgtcttg 210
 gaaagtcttt tatagaaggt accagatttc aatggaacag ctggaaaaac 1000
 ttcaggggac attgtttctcc acagaagagg agccctctaa gctttctgta 1050
 caaaaactac gagcccttca gctctcaat cagcgcctgg tctttgcttc 1100
 tttcatccaa gcaggatctt cgtataccac aggtgaaatg cttaqtctag 1150
 gtataggaat ctgtgttggc tgtctctgcc ctctctggc tgtttatttc 1200
 attgctagaa agattcggaa gaagagcctg gaaaaaccga agagtgtggt 1250
 ctccacctca gcacaagcca cgaactgagc ataaattctt tctcagatac 1300
 catggatctg gatgacttcc cttaatgctt atcaggaagc ctctaaaatg 1350
 ggggtgtagga tctggccaga aacactgtag gagtactaag cagatgtctt 1400
 acttcccttg gacatctctt agagaggaat ggaccacagg tgtcattcca 1450
 ggaagaactg cagagccttc agcctctcca aacatgttag aggaaatgag 1500
 gaaatccttg tgttgtaat gcagagacca aactctgttt agttgcaggg 1550
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
 tttccctaga tatactgggg gatctctctt taggataaag agttgctgtt 1650
 gaagtttat atttttgac aatatatttg gaaattaaag tttctgactt 1700
 t 1701

<210> 423
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
 1 5 10 15
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80	85	90
Pro Ser Thr Leu Tyr 95	Leu Gly Gly Leu Pro Arg Lys Tyr Val 100	Ala 105
Ala Gln Leu His 110	Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly 115	120
Ser Glu His Gln 125	Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His 130	135
Ile Val His Tyr 140	Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala 145	150
Ala Glu Arg Pro 155	Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu 160	165
Val Gly Glu Thr 170	Lys Asn Ile Ala Tyr Gln His Ile Leu Ser His 175	180
Leu His Glu Val 185	Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro 190	195
Phe Asn Leu Arg 200	Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe 205	210
Arg Tyr Asn Gly 215	Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val 220	225
Leu Trp Thr Val 230	Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln 235	240
Leu Glu Lys Leu 245	Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro 250	255
Ser Lys Leu Leu 260	Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn 265	270
Gln Arg Met Val 275	Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr 280	285
Thr Thr Gly Glu 290	Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly 295	300
Cys Leu Cys Leu 305	Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile 310	315
Arg Lys Lys Arg 320	Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser 325	330
Ala Gln Ala Thr 335	Thr Glu Ala	

<210> 424
 <211> 16
 <212> CNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaagtcgc tggccagc 18

<10> 425
<11> 18
<12> DNA
<13> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
ccgcatctgc ctgctgta 18

<10> 426
<11> 24
<12> DNA
<13> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<10> 427
<11> 45
<12> DNA
<13> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaacacca tgatacccta ctgaacaccg aatccccctgg aagcc 45

<10> 428
<11> 1073
<12> DNA
<13> Homo sapiens

<400> 428
aatttttcac cagagtaaac ttgagaaacc aactggacat tgactattgt 50
acattttgat tctatgacac aaaggtayca atctgaaaca tgaggagtar 100
gattttastg ttttgttttc taagatcaat tgggtcatta ccacatctca 150

aatgtgtttt ggaactctct cccacaaaac tggctcaga tcacagaaac 200
 ctacacaaac aacagcagtc aaatcaggtc tttctttctt taagtctgat 250
 acatttaaca cagatgtctc caatgggggc agatctgcac ctgttaaatc 300
 ctgctgcagg aatgacact ggtaccacga cccacccatt gaacctggga 350
 ggttgatg tacaacagca actgcaccca catgtgttac caatttttgt 400
 cacacactt ggagcccagg gaactatctt aagctcagag gaattggcac 450
 aaattctac gagctctcct atccattctt tgttcccgga aggcattctg 500
 cccacagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggggga gcagggtgtt atctggcac ccagggaacc ccagcaggcc 600
 gctcccaac tccagtggc acagatgacg actttgcagt gaccacccct 650
 gcaggctcc aaaggagcac acatgcctc gaggaagcca ccacagaatc 700
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagtgcct 750
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
 gatgacaca cattggatag tottagaaga aattaattct taatttaact 850
 gaaatattc ttgaaattc agaaaatatg ttctatgtag agaattccaa 900
 cttttcaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgcttctt ggatgatatg catattaaaa catatttgga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 419
 <211> 249
 <212> PET
 <213> Homo sapiens

<100> 419
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1 5 10 15
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
 20 25 30
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
 35 40 45
 Val Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
 50 55 60
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
 65 70

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
				200					205					

<210 - 430
 <211 - 1257
 <212 - DNA
 <213 - Homo Sapien

<400 - 430
 ggagagagggc ggggggggtga aaggggcatt gatgcagcct gggggggcct 50
 cggagcggggc cggagccaga cgcctgaccac gttcctctcc tgggtctcct 100
 ccgcctccag ctcggcgctg cccggccagcc gggagccatg ccaccccagg 150
 gccccggccc ctccccgagcgg cggctccggcg gctcctctgt gctcctgctg 200
 ctgcagctgc cccggccgctc gagcgccctct gagatcccca aggggaagca 250
 aaaggccagc ctcggccaga gggaggtggt ggaacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag cctgggggac 350
 aatgttatcc cgggtacacc tgggatccca ggtcgggcatg gattcaaagg 400
 agaaaaagggg gaatgtctga gggaaaagctt tgaggagtc tggacaccca 450
 actacaagca gtgttcctgg agttcattga attatcgcat aatctctggg 500
 aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgtcttaag 550
 agtttgttgc aatgggtcac ttccgtctaaa atgcacaaat ccattctgtc 600
 aactctcata ttccacattc aatggagctg aatctccagc aatctctctc 650

taatttattt aaacaaagga aacattaaa tgaattaaa 700
 cataggaatt cttctgtgga aggaatttga gaaggaattg 750
 agtgaatgtt gctatctggg ttggaatttg ttcagattac 800
 atgctttctac tggatggaat tcaatttctc gaatcattat 850
 ccaaaataaa tgccttaatt ttcatttget aactcttttt 900
 ttggaatggt tcaactaaat qacattttta ataagtttat 950
 gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
 ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
 aatcttttc aatatttttt ttagttgggt agaatacttt cttcatactc 1100
 aattctctc aactataat ttggaatatt gttgtggtct ttgtttttt 1150
 ctctagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
 aatttgtaaa tgttaagaat ttttttata tctgttaaatt aaaaattatt 1250
 tccaaca 1257

<210> 431
 <211> 243
 <212> PRT
 <213> Homo Sapien

<400> 431
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135

Ala	Leu	Arg	Val	Leu	Ile	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Gln	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Phe	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Asa	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence

<400> 432
 ...ggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<400> 433
 ...ccaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<400> 434
 ...atgaacatg tacaaggaca c 21

<210> 435

<111> 19
<111> DNA
<111> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 435
ccaccctgta ccaccatgt 19

<210> 436
<211> 24
<211> DNA
<211> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 436
actccaggca ccactctgttc tccc 24

<210> 437
<211> 19
<211> DNA
<211> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 437
gaagcgtggc attcaagtc 19

<210> 438
<211> 19
<211> DNA
<211> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
gaagcgtggc aaggaagaa 19

<210> 439
<211> 21
<211> DNA
<211> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
cagccaccct ccagtcgaag g 21

<210> 440
<211> 19
<211> DNA
<211> Artificial Sequence

<10> Synthetic oligonucleotide probe

<11> 440

tttttggttt ttggagaga 19

<110> 441

<111> 20

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 441

ttgtgcctca gaggaccaat 20

<110> 442

<111> 25

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 442

ttctccatca ctctccctag ctcca 25

<110> 443

<111> 24

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 443

tttggcaggag ttaaagttcc aaga 24

<110> 444

<111> 18

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 444

aaaggacacc gggatgtg 18

<110> 445

<111> 26

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 445
 ctcttcaact ctctcagga aa vsp 26

 <210> 446
 <211> 13
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 446
 cttttctaga tgagatgga ga 22

 <210> 447
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 447
 caggactgag cgtttgttta 20

 <210> 448
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 448
 cgaagcgcga agtaccggac c 21

 <210> 449
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 449
 ccagacctca gccaggaa 18

 <210> 450
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 450
 cttatctaga cttcttta 18

<110> 451
 <111> 23
 <112> DNA
 <113> Artificial Sequence

 <200>
 <210> Synthetic oligonucleotide probe

 <400> 451
 atgacaagc attttttctga atc 23

 <110> 452
 <111> 26
 <112> DNA
 <113> Artificial Sequence

 <200>
 <210> Synthetic oligonucleotide probe

 <400> 452
 atccccct cctttttctt ttgttt 26

 <110> 453
 <111> 18
 <112> DNA
 <113> Artificial Sequence

 <200>
 <210> Synthetic oligonucleotide probe

 <400> 453
 atgtgtgcc cacagtga 18

 <110> 454
 <111> 21
 <112> DNA
 <113> Artificial Sequence

 <200>
 <210> Synthetic oligonucleotide probe

 <400> 454
 ccatgectgc tcagccaaga a 21

 <110> 455
 <111> 23
 <112> DNA
 <113> Artificial Sequence

 <200>
 <210> Synthetic oligonucleotide probe

 <400> 455
 atgaaatct gaaagctac att 23

 <110> 456
 <111> 21
 <112> DNA

<119> Artificial Sequence

<120>
<121> Synthetic oligonucleotide probe

<122>
<123> gaccagttt 20

<124>
<125>
<126>
<127>
<128> Artificial Sequence

<129>
<130> Synthetic oligonucleotide probe

<131>
<132> ctactatga cctactttt cc 22

<133> 15c
<134> 18
<135> DNA
<136> Artificial Sequence

<137>
<138> Synthetic oligonucleotide probe

<139> 458
<140> ctacagctgc ccttgta 18

<141> 459
<142> 22
<143> DNA
<144> Artificial Sequence

<145>
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<147> 459
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